

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 23, 2005, 20:48:35 ; Search time 132 Seconds

(without alignment)  
1189.967 Million cell updates/sec

Title: US-10-621-485A-1

Perfect score: 2550

Sequence: 1 MSDVAIVKEGWLHKGVEIK.....VDSRRPHFPQSYASGTA 480

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description        |
|------------|-------|-------|--------|----|--------------------|
| 1          | 2550  | 100.0 | 480    | 17 | US-10-621-485A-1   |
| 2          | 2544  | 99.8  | 492    | 10 | US-09-955-999-96   |
| 3          | 2544  | 99.8  | 480    | 9  | US-09-771-161A-223 |
| 4          | 2544  | 99.8  | 480    | 9  | US-09-970-000-4    |
| 5          | 2544  | 99.8  | 480    | 10 | US-09-526-043-14   |
| 6          | 2544  | 99.8  | 480    | 14 | US-10-060-065-18   |
| 7          | 2544  | 99.8  | 480    | 14 | US-10-059-585-39   |
| 8          | 2544  | 99.8  | 480    | 15 | US-10-394-322A-1   |
| 9          | 2544  | 99.8  | 480    | 15 | US-10-217-574-31   |
| 10         | 2544  | 99.8  | 480    | 15 | US-10-217-555-31   |
| 11         | 2544  | 99.8  | 480    | 16 | US-10-701-490-4    |
| 12         | 2544  | 99.8  | 480    | 16 | US-10-713-678-2    |
| 13         | 2544  | 99.8  | 480    | 16 | US-10-746-545-36   |

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|----|--------|------|-----|----|--------------------|--------------------|
| 14 | 2544   | 99.8 | 524 | 14 | US-10-103-256-11   | Sequence 11, Appl  |
| 15 | 2544   | 99.8 | 524 | 15 | US-10-365-348-11   | Sequence 11, Appl  |
| 16 | 2544   | 99.8 | 726 | 14 | US-10-072-036-71   | Sequence 71, Appl  |
| 17 | 2544   | 99.8 | 727 | 14 | US-10-072-036-139  | Sequence 139, Appl |
| 18 | 2509   | 98.4 | 480 | 16 | US-10-713-678-6    | Sequence 6, Appl   |
| 19 | 2494   | 97.8 | 480 | 9  | US-09-205-658-157  | Sequence 157, Appl |
| 20 | 2494   | 97.8 | 480 | 10 | US-09-963-693-157  | Sequence 157, Appl |
| 21 | 2161.5 | 84.8 | 417 | 16 | US-10-713-678-4    | Sequence 4, Appl   |
| 22 | 2128.5 | 83.5 | 488 | 16 | US-10-322-281-413  | Sequence 413, Appl |
| 23 | 2126.5 | 83.4 | 480 | 10 | US-09-526-043-13   | Sequence 13, Appl  |
| 24 | 2126.5 | 83.4 | 480 | 15 | US-10-394-568-11   | Sequence 11, Appl  |
| 25 | 2126.5 | 83.4 | 481 | 15 | US-10-394-322A-2   | Sequence 2, Appl   |
| 26 | 2126.5 | 83.4 | 481 | 15 | US-10-217-574-32   | Sequence 32, Appl  |
| 27 | 2126.5 | 83.4 | 481 | 15 | US-10-217-555-32   | Sequence 32, Appl  |
| 28 | 2126.5 | 83.4 | 564 | 16 | US-10-322-281-416  | Sequence 416, Appl |
| 29 | 2105.5 | 82.6 | 479 | 9  | US-09-771-161A-247 | Sequence 247, Appl |
| 30 | 2105.5 | 82.6 | 479 | 9  | US-09-771-161A-248 | Sequence 248, Appl |
| 31 | 2105.5 | 82.6 | 479 | 15 | US-10-394-322A-3   | Sequence 3, Appl   |
| 32 | 2105.5 | 82.6 | 479 | 15 | US-10-217-574-33   | Sequence 33, Appl  |
| 33 | 2105.5 | 82.6 | 479 | 15 | US-10-217-555-33   | Sequence 33, Appl  |
| 34 | 2105.5 | 82.6 | 465 | 10 | US-09-526-043-2    | Sequence 2, Appl   |
| 35 | 2008.5 | 78.8 | 465 | 15 | US-10-394-568-2    | Sequence 12, Appl  |
| 36 | 2008.5 | 78.8 | 465 | 15 | US-10-394-568-12   | Sequence 12, Appl  |
| 37 | 2008.5 | 78.8 | 465 | 15 | US-09-526-043-17   | Sequence 17, Appl  |
| 38 | 1989.5 | 78.0 | 454 | 10 | US-10-116-722A-7   | Sequence 7, Appl   |
| 39 | 1692   | 66.4 | 320 | 14 | US-10-116-722A-5   | Sequence 5, Appl   |
| 40 | 1671   | 65.5 | 320 | 14 | US-10-116-722A-8   | Sequence 8, Appl   |
| 41 | 1573   | 61.7 | 300 | 16 | US-10-664-421-84   | Sequence 24, Appl  |
| 42 | 1552.5 | 60.9 | 335 | 16 | US-10-746-545-24   | Sequence 37, Appl  |
| 43 | 1552.5 | 60.9 | 335 | 16 | US-10-746-545-37   | Sequence 21, Appl  |
| 44 | 1552.5 | 60.9 | 336 | 15 | US-10-217-574-21   | Sequence 21, Appl  |
| 45 | 1552.5 | 60.9 | 336 | 15 | US-10-217-555-21   | Sequence 21, Appl  |

ALIGNMENTS

RESULT 1  
US-10-621-485A-1  
; Sequence 1, Application US/10621485A  
; Publication No. US20050014682A1  
; GENERAL INFORMATION:  
; APPLICANT: MUECKLER, MIKE  
; APPLICANT: HRESKO, RICHARD  
; APPLICANT: MURATA, HARUHIKO  
; TITLE OF INVENTION: CELL-FREE ASSAY FOR INSULIN SIGNALING  
; FILE REFERENCE: 56029/41936  
; CURRENT APPLICATION NUMBER: US/10/621.485A  
; CURRENT FILING DATE: 2003-07-16  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: Patent In Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-621-485A-1

|                       |         |  |        |                                 |
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| Query Match           | 100.0%; | Score 2550;  | DB 17; | Length 480;                     |
| Best Local Similarity | 100.0%; | Pred. No. 2.6e-165;                                      |        |                                 |
| Matches               | 480;    | Conservative   | 0;     | Mismatches 0; Indels 0; Gaps 0; |
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| Db                    | 1       | MSDVAIVKEGWLHKGVEIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC  | 60     |                                 |
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| Qy                    | 121     | RSGSPDSNGAEEMVSLAKPKHRTVWNEFEYLLKLGKTFGKVLVKEKATGYAMKI   | 180    |                                 |
| Db                    | 121     | RSGSPDSNGAEEMVSLAKPKHRTVWNEFEYLLKLGKTFGKVLVKEKATGYAMKI   | 180    |                                 |

Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELPFHLS 240  
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Qy 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVYRDLEMLDKDGHIKITDFGLCKEGI 300  
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Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPQDDSMCEVDSERRRPHFPQFSYASGTA 480

RESULT 2  
US-09-955-999-96  
; Sequence 96, Application US/09955999  
; Publication No. US20030036505A1  
; GENERAL INFORMATION:  
; APPLICANT: Barash et al.  
; TITLE OF INVENTION: Signal Transduction Pathway Component Polynucleotides, Polypeptides  
; FILE REFERENCE: PT086F1  
; CURRENT APPLICATION NUMBER: US/09/955,999  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/234,997  
; PRIOR FILING DATE: 2000-09-25  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: Patent in ver. 2.0  
; SEQ ID NO 96  
; LENGTH: 492  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-955-999-96

Query Match 100.0%; Score 2550; DB 10; Length 492;  
Best Local Similarity 100.0%; Pred. No. 2,7e-165;  
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 73 QLMKTERPRNTFIIRCLQWTVIERTPHVETPEEREETTAIQTVDGLKKQEEEMDF 132  
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Db 433 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPQDDSMCEVDSERRRPHFPQFSYASGTA 492

RESULT 3  
US-09-771-161A-223  
; Sequence 223, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 223  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-223

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Best Local Similarity 99.8%; Pred. No. 6,7e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 4  
US-09-970-000-4  
; Sequence 4, Application US/09970000  
; Patent No. US20020127214A1  
; GENERAL INFORMATION:  
; APPLICANT: Hemmings, Brian Arthur

TITLE OF INVENTION: Rac-Protein Kinase as Therapeutic Agent  
; Or In Diagnostics  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. US2002012714A1artis Patent and Trademark Department  
; STREET: 564 Morris Avenue  
; CITY: Summit  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07901-1027  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/970,000  
; FILING DATE: 03-Oct-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/068,702  
; FILING DATE: 13-May-1998  
; APPLICATION NUMBER: PCT/EP96/04810  
; FILING DATE: 11-May-1996  
; APPLICATION NUMBER: GB 9523379.7  
; FILING DATE: 16-No. US2002012714A1-1995  
; APPLICATION NUMBER: GB 9525704.4  
; FILING DATE: 15-Dec-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Furman, Diane E.  
; REGISTRATION NUMBER: 31,104  
; REFERENCE/DOCKET NUMBER: 4-20635/A/PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 522-6924  
; TELEFAX: (908) 522-6955  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 480 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-970-000-4

Query Match 99.8%; Score 2544; DB 9; Length 480;  
Best Local Similarity 99.8%; Pred. No. 6.7e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MSDVAIVKEGWLKRGGEYIKTRPRYFLKNDGTFIGYKERPDQVDDQREAPLNFSVAQC 60  
Db 1 MSDVAIVKEGWLKRGGEYIKTRPRYFLKNDGTFIGYKERPDQVDDQREAPLNFSVAQC 60  
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Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHETPEEREETTAIQTVDGLKKQBEEMDF 120  
Qy 121 RSGSPSDNSGAEEMVSLAKPKHRTVMNEFYLLKLGKGTGKVLVKEKATGRYAMKI 180  
Db 121 RSGSPSDNSGAEEMVSLAKPKHRTVMNEFYLLKLGKGTGKVLVKEKATGRYAMKI 180  
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Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Qy 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVYRDLENLMDKDGHIKITDGLCKEGI 300  
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Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDSDMECVDSERRRPHFPQSASGTA 480

Db 361 ILMBEIRPRTLGPPEAKSLLSGLLKDDPKQRLGGSEDAKEIMQHRFFAGIWMQHVYEKK 420  
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RESULT 5  
US-09-526-043-14  
; Sequence 14, Application US/09526043  
; Publication No. US20030100049A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Kun  
; APPLICANT: Pagnoni, Marco  
; APPLICANT: Clark, Kenneth  
; APPLICANT: Ivashchenko, Yuri  
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF  
; FILE REFERENCE: A3278A-US  
; CURRENT APPLICATION NUMBER: US/09/526,043  
; CURRENT FILING DATE: 2000-03-14  
; EARLIER APPLICATION NUMBER: 60/125,108  
; EARLIER FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-526-043-14

Query Match 99.8%; Score 2544; DB 10; Length 480;  
Best Local Similarity 99.8%; Pred. No. 6.7e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MSDVAIVKEGWLKRGGEYIKTRPRYFLKNDGTFIGYKERPDQVDDQREAPLNFSVAQC 60  
Db 1 MSDVAIVKEGWLKRGGEYIKTRPRYFLKNDGTFIGYKERPDQVDDQREAPLNFSVAQC 60  
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Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHETPEEREETTAIQTVDGLKKQBEEMDF 120  
Qy 121 RSGSPSDNSGAEEMVSLAKPKHRTVMNEFYLLKLGKGTGKVLVKEKATGRYAMKI 180  
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Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Qy 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVYRDLENLMDKDGHIKITDGLCKEGI 300  
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Qy 361 ILMBEIRPRTLGPPEAKSLLSGLLKDDPKQRLGGSEDAKEIMQHRFFAGIWMQHVYEKK 420  
Db 361 ILMBEIRPRTLGPPEAKSLLSGLLKDDPKQRLGGSEDAKEIMQHRFFAGIWMQHVYEKK 420  
Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDSDMECVDSERRRPHFPQSASGTA 480  
Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDSDMECVDSERRRPHFPQSASGTA 480

RESULT 6  
US-10-060-065-18  
; Sequence 18, Application US/10060065  
; Publication No. US20030017480A1  
; GENERAL INFORMATION:  
; APPLICANT: Toshio Ota

APPLICANT: Takao Isogai  
APPLICANT: Tetsuo Nishikawa  
APPLICANT: Koji Hayaashi  
APPLICANT: Kaoru Otsuka  
APPLICANT: Jun-ichi Yamamoto  
APPLICANT: Shizuko Ishii  
APPLICANT: Tomoyasu Sugiyama  
APPLICANT: Ai Wakamatsu  
APPLICANT: Keiichi Nagai  
APPLICANT: Tetsuji Otsuki  
APPLICANT: Shin-ichi Funahashi  
APPLICANT: Chiaki Senoo  
APPLICANT: Jun-ichi Nezu  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE  
FILE REFERENCE: 06501-099002  
CURRENT APPLICATION NUMBER: US/10/060,065  
CURRENT FILING DATE: 2002-01-29  
PRIOR APPLICATION NUMBER: PCT/JP00/05061  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: US 60/159,590  
PRIOR FILING DATE: 1999-10-18  
PRIOR APPLICATION NUMBER: US 60/183,322  
PRIOR FILING DATE: 2000-02-17  
PRIOR APPLICATION NUMBER: JP 11-248036  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: JP 2000-118776  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: JP 2000-183767  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: JP 2000-241899  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 18  
LENGTH: 480  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-060-065-18

Query Match 99.8%; Score 2544; DB 14; Length 480;  
Best Local Similarity 99.8%; Pred. No. 6.7e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MSDVAIVKEGWLHKGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60  
Db 1 MSDVAIVKEGWLHKGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60  
Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKQEEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKQEEEMDF 120  
Qy 121 RSGSPDSNGAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Db 121 RSGSPDSNGAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Qy 181 LKKEVIVAKDEVATHTLNRVQLNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Db 181 LKKEVIVAKDEVATHTLNRVQLNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Qy 241 RERVFSDDRARFYGAIEIVSALDYLHSEKNVYVRDLKLENMLDKDGHKITDGLCKEGI 300  
Db 241 RERVFSDDRARFYGAIEIVSALDYLHSEKNVYVRDLKLENMLDKDGHKITDGLCKEGI 300  
Qy 301 KDGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYNQDHEKLP 360  
Db 301 KDGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYNQDHEKLP 360  
Qy 361 ILMBEIRPRTLGPPEAKSLLSGLLKQPKQRLGGSEDAKEIMQRRFFAGVWQHVYEKK 420  
Db 361 ILMBEIRPRTLGPPEAKSLLSGLLKQPKQRLGGSEDAKEIMQRRFFAGVWQHVYEKK 420  
Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMTITPPDQDSDMECVDSERRRPHFPQFSYSASGTA 480  
Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMTITPPDQDSDMECVDSERRRPHFPQFSYSASGTA 480

Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMTITPPDQDSDMECVDSERRRPHFPQFSYSASSTA 480  
RESULT 7  
US-10-059-585-39  
Sequence 39, Application US/10059585  
Publication No. US20030082776A1  
GENERAL INFORMATION:  
APPLICANT: Ota, Toshio  
APPLICANT: Isogai, Takao  
APPLICANT: Nishikawa, Tetsuo  
APPLICANT: Hayaashi, Koji  
APPLICANT: Otsuka, Kaoru  
APPLICANT: Yamamoto, Jun-ichi  
APPLICANT: Ishii, Shizuko  
APPLICANT: Sugiyama, Tomoyasu  
APPLICANT: Wakamatsu, Ai  
APPLICANT: Nagai, Keiichi  
APPLICANT: Otsuki, Tetsuji  
APPLICANT: Funahashi, Shin-ichi  
APPLICANT: Senoo, Chiaki  
APPLICANT: Nezu, Jun-ichi  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE  
FILE REFERENCE: 06501-098001  
CURRENT APPLICATION NUMBER: US/10/059,585  
CURRENT FILING DATE: 2002-01-29  
PRIOR APPLICATION NUMBER: PCT/JP00/05060  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: US 60/183,322  
PRIOR FILING DATE: 2000-02-17  
PRIOR APPLICATION NUMBER: US 60/159,590  
PRIOR FILING DATE: 1999-10-18  
PRIOR APPLICATION NUMBER: JP 2000-118776  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: JP 2000-183767  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: JP 11-248036  
PRIOR FILING DATE: 1999-07-29  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 39  
LENGTH: 480  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-059-585-39

Query Match 99.8%; Score 2544; DB 14; Length 480;  
Best Local Similarity 99.8%; Pred. No. 6.7e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MSDVAIVKEGWLHKGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60  
Db 1 MSDVAIVKEGWLHKGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60  
Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKQEEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKQEEEMDF 120  
Qy 121 RSGSPDSNGAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Db 121 RSGSPDSNGAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Qy 181 LKKEVIVAKDEVATHTLNRVQLNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Db 181 LKKEVIVAKDEVATHTLNRVQLNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Qy 241 RERVFSDDRARFYGAIEIVSALDYLHSEKNVYVRDLKLENMLDKDGHKITDGLCKEGI 300  
Db 241 RERVFSDDRARFYGAIEIVSALDYLHSEKNVYVRDLKLENMLDKDGHKITDGLCKEGI 300  
Qy 301 KDGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYNQDHEKLP 360  
Db 301 KDGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYNQDHEKLP 360

Db 301 KGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
Qy 361 LMEEIRPRTLGPPEAKSLGSLKDKPKQKQLGGSEDAKEIMQHRFPFAGIWHQVYVYKK 420  
Db 361 LMEEIRPRTLGPPEAKSLGSLKDKPKQKQLGGSEDAKEIMQHRFPFAGIWHQVYVYKK 420  
Qy 421 LSPFPKQVTSSETDTRYDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480  
Db 421 LSPFPKQVTSSETDTRYDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480

RESULT 8  
US-10-394-322A-1  
; Sequence 1, Application US/10394322A  
; Publication No. US20030232391A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.  
; APPLICANT: Prescott, John C.  
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS  
; FILE REFERENCE: 39750-0006 US  
; CURRENT APPLICATION NUMBER: US/10/394,322A  
; CURRENT FILING DATE: 2003-03-20  
; PRIOR FILING DATE: 2003-03-20  
; PRIOR FILING DATE: 2003-03-21  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-394-322A-1

Query Match 99.8%; Score 2544; DB 15; Length 480;  
Best Local Similarity 99.8%; Pred. No. 6.7e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNNFSVAQC 60  
Db 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNNFSVAQC 60

Qy 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120

Qy 121 RSGSPDSNGAEEMVSLAKPKRVTWNEPEYLLKLGKTFGKVLVKEKATGRYAMKI 180  
Db 121 RSGSPDSNGAEEMVSLAKPKRVTWNEPEYLLKLGKTFGKVLVKEKATGRYAMKI 180

Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSPQTHDRLCFVMEYANGGELFFHLS 240  
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSPQTHDRLCFVMEYANGGELFFHLS 240

Qy 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Db 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300

Qy 301 KGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
Db 301 KGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360

Qy 361 LMEEIRPRTLGPPEAKSLGSLKDKPKQKQLGGSEDAKEIMQHRFPFAGIWHQVYVYKK 420  
Db 361 LMEEIRPRTLGPPEAKSLGSLKDKPKQKQLGGSEDAKEIMQHRFPFAGIWHQVYVYKK 420

Qy 421 LSPFPKQVTSSETDTRYDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480  
Db 421 LSPFPKQVTSSETDTRYDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480

RESULT 9  
US-10-217-574-31  
; Sequence 31, Application US/10217574  
; Publication No. US20040005687A1

; GENERAL INFORMATION:  
; APPLICANT: Barford, David  
; APPLICANT: Yang, Jing  
; APPLICANT: Hemmings, Brian A  
; APPLICANT: Cron, Peter D  
; TITLE OF INVENTION: Kinase Crystal Structures  
; FILE REFERENCE: 44237  
; CURRENT APPLICATION NUMBER: US/10/217,574  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR FILING DATE: 2002-05-01  
; PRIOR FILING DATE: 2002-05-01  
; PRIOR FILING DATE: 2002-07-12  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-217-574-31

Query Match 99.8%; Score 2544; DB 15; Length 480;  
Best Local Similarity 99.8%; Pred. No. 6.7e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNNFSVAQC 60  
Db 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNNFSVAQC 60

Qy 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120

Qy 121 RSGSPDSNGAEEMVSLAKPKRVTWNEPEYLLKLGKTFGKVLVKEKATGRYAMKI 180  
Db 121 RSGSPDSNGAEEMVSLAKPKRVTWNEPEYLLKLGKTFGKVLVKEKATGRYAMKI 180

Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSPQTHDRLCFVMEYANGGELFFHLS 240  
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSPQTHDRLCFVMEYANGGELFFHLS 240

Qy 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Db 241 RERVSEDRARFYGAIEVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300

Qy 301 KGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
Db 301 KGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360

Qy 361 LMEEIRPRTLGPPEAKSLGSLKDKPKQKQLGGSEDAKEIMQHRFPFAGIWHQVYVYKK 420  
Db 361 LMEEIRPRTLGPPEAKSLGSLKDKPKQKQLGGSEDAKEIMQHRFPFAGIWHQVYVYKK 420

Qy 421 LSPFPKQVTSSETDTRYDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480  
Db 421 LSPFPKQVTSSETDTRYDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480

RESULT 10  
US-10-217-555-31  
; Sequence 31, Application US/10217555  
; Publication No. US20040009569A1  
; GENERAL INFORMATION:  
; APPLICANT: Barford, David  
; APPLICANT: Hemmings, Brian A  
; APPLICANT: Cron, Peter D  
; TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for  
; TITLE OF INVENTION: Kinase Activation  
; FILE REFERENCE: 44236  
; CURRENT APPLICATION NUMBER: US/10/217,555

```

; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 31
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-217-555-31

Query Match          99.8%; Score 2544; DB 15; Length 480;
Best Local Similarity 99.8%; Pred. No. 6.7e-165;
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKRPQDVQDQREAPLNNFSAQC 60
Db 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKRPQDVQDQREAPLNNFSAQC 60

Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120

Qy 121 RSGSPDNGSAGEMEVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180
Db 121 RSGSPDNGSAGEMEVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180

Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMYANGGELPFHLS 240
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMYANGGELPFHLS 240

Qy 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVYRDLEMLDKDGHIKITDFGLCKEGI 300
Db 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVYRDLEMLDKDGHIKITDFGLCKEGI 300

Qy 301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWGLGVVYMMCGRLPFYVQDHEKLFEL 360
Db 301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWGLGVVYMMCGRLPFYVQDHEKLFEL 360

Qy 361 LMEEIRFPRTLGPPEAKSLGLLKKDPKQRLGGSEDAKEIMQHRFFAGIVMHHVYEEK 420
Db 361 LMEEIRFPRTLGPPEAKSLGLLKKDPKQRLGGSEDAKEIMQHRFFAGIVMHHVYEEK 420

Qy 421 LSPFPKQVTSSETDTRFYDEEFTAQMITITPPDQDSDMECVDSRRPFPQFSYASGTA 480
Db 421 LSPFPKQVTSSETDTRFYDEEFTAQMITITPPDQDSDMECVDSRRPFPQFSYASGTA 480

RESULT 12
US-10-713-678-2
; Sequence 2, Application US/10713678
; Publication No. US20040122077A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/10/713,678
; CURRENT FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-713-678-2

Query Match          99.8%; Score 2544; DB 16; Length 480;
Best Local Similarity 99.8%; Pred. No. 6.7e-165;
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKRPQDVQDQREAPLNNFSAQC 60
Db 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKRPQDVQDQREAPLNNFSAQC 60

Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVDGLKKQEEEMDF 120

Qy 121 RSGSPDNGSAGEMEVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180
Db 121 RSGSPDNGSAGEMEVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180

Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMYANGGELPFHLS 240
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMYANGGELPFHLS 240

Qy 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVYRDLEMLDKDGHIKITDFGLCKEGI 300
Db 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVYRDLEMLDKDGHIKITDFGLCKEGI 300

Qy 301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWGLGVVYMMCGRLPFYVQDHEKLFEL 360
Db 301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWGLGVVYMMCGRLPFYVQDHEKLFEL 360

Qy 361 LMEEIRFPRTLGPPEAKSLGLLKKDPKQRLGGSEDAKEIMQHRFFAGIVMHHVYEEK 420
Db 361 LMEEIRFPRTLGPPEAKSLGLLKKDPKQRLGGSEDAKEIMQHRFFAGIVMHHVYEEK 420

Qy 421 LSPFPKQVTSSETDTRFYDEEFTAQMITITPPDQDSDMECVDSRRPFPQFSYASGTA 480
Db 421 LSPFPKQVTSSETDTRFYDEEFTAQMITITPPDQDSDMECVDSRRPFPQFSYASGTA 480

RESULT 11
US-10-701-490-4
; Sequence 4, Application US/10701490
; Publication No. US20040106141A1
; GENERAL INFORMATION:
; APPLICANT: PAUL S. MISCHER
; APPLICANT: CHARLES L. SAWYERS
; APPLICANT: BRADLEY L. SMITH
; APPLICANT: KATHERINE CROSBY
; TITLE OF INVENTION: METHODS AND MATERIALS FOR EXAMINING
; FILE REFERENCE: GAC 30435.148USU1
; CURRENT APPLICATION NUMBER: US/10/701,490
; CURRENT FILING DATE: 2003-11-05
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-701-490-4

```

Db 121 RSGSPDNGSGAEVSLAKPKHRTWNEFYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Qy 241 RERVSEDRARFYGAETVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Db 241 RERVSEDRARFYGAETVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Qy 301 KDGATMTKTCGTPPYLAPEVLEDNDYGRAVDWGLGVVYEMMCGRLPFYFNQDHEKLFEL 360  
Db 301 KDGATMTKTCGTPPYLAPEVLEDNDYGRAVDWGLGVVYEMMCGRLPFYFNQDHEKLFEL 360  
Qy 361 ILMEIIRPRTLGPPEAKSLLSGLLKOPKORLGGGSEDAKEIMQHRFPFAGIWMQHVYK 420  
Db 361 ILMEIIRPRTLGPPEAKSLLSGLLKOPKORLGGGSEDAKEIMQHRFPFAGIWMQHVYK 420  
Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYSASGTA 480  
Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYSASGTA 480

## RESULT 13

US-10-746-545-36  
; Sequence 36, Application US/10746545  
; Publication No. US20040171075A1  
; GENERAL INFORMATION:  
; APPLICANT: Deciphra Pharmaceuticals, Inc.  
; APPLICANT: Flynn, Daniel L.  
; APPLICANT: Petillo, Peter A.  
; TITLE OF INVENTION: MODULATION OF PROTEIN FUNCTIONALITIES  
; FILE REFERENCE: 34475  
; CURRENT APPLICATION NUMBER: US/10746.545  
; CURRENT FILING DATE: 2003-12-24  
; PRIOR APPLICATION NUMBER: US 60/437,487  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 36  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-746-545-36

Query Match 99.8%; Score 2544; DB 16; Length 480;  
Best Local Similarity 99.8%; Pred. No. 6.7e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGGEYIKTWPRYFLKNDGTFIGYKERPDQVQDQREAPLNFSVAQC 60  
Db 1 MSDVAIVKEGWLHKGGEYIKTWPRYFLKNDGTFIGYKERPDQVQDQREAPLNFSVAQC 60  
Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEREETWTAIQTVDGLKKQBEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEREETWTAIQTVDGLKKQBEEMDF 120  
Qy 121 RSGSPDNGSGAEVSLAKPKHRTWNEFYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Db 121 RSGSPDNGSGAEVSLAKPKHRTWNEFYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Qy 241 RERVSEDRARFYGAETVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Db 241 RERVSEDRARFYGAETVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Qy 301 KDGATMTKTCGTPPYLAPEVLEDNDYGRAVDWGLGVVYEMMCGRLPFYFNQDHEKLFEL 360  
Db 301 KDGATMTKTCGTPPYLAPEVLEDNDYGRAVDWGLGVVYEMMCGRLPFYFNQDHEKLFEL 360

Qy 361 ILMEIIRPRTLGPPEAKSLLSGLLKOPKORLGGGSEDAKEIMQHRFPFAGIWMQHVYK 420  
Db 361 ILMEIIRPRTLGPPEAKSLLSGLLKOPKORLGGGSEDAKEIMQHRFPFAGIWMQHVYK 420  
Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYSASGTA 480  
Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYSASGTA 480

RESULT 14  
US-10-103-256-11  
; Sequence 11, Application US/10103256  
; Publication No. US20030181366A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Luo, Yan  
; APPLICANT: Giranda, Vincent L.  
; APPLICANT: Smith, Richard A.  
; APPLICANT: Richardson, Paul L.  
; APPLICANT: Hutchins, Charles  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF AKT AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 6904.US.O1  
; CURRENT APPLICATION NUMBER: US/10/103.256  
; CURRENT FILING DATE: 2002-07-09  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 524  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-103-256-11

Query Match 99.8%; Score 2544; DB 14; Length 524;  
Best Local Similarity 99.8%; Pred. No. 7.4e-165;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGGEYIKTWPRYFLKNDGTFIGYKERPDQVQDQREAPLNFSVAQC 60  
Db 45 MSDVAIVKEGWLHKGGEYIKTWPRYFLKNDGTFIGYKERPDQVQDQREAPLNFSVAQC 104  
Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEREETWTAIQTVDGLKKQBEEMDF 120  
Db 105 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEREETWTAIQTVDGLKKQBEEMDF 164  
Qy 121 RSGSPDNGSGAEVSLAKPKHRTWNEFYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Db 165 RSGSPDNGSGAEVSLAKPKHRTWNEFYLLKLGKTFGKVLVKEKATGRYYAMKI 224  
Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
Db 225 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 284  
Qy 241 RERVSEDRARFYGAETVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Db 285 RERVSEDRARFYGAETVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 344  
Qy 301 KDGATMTKTCGTPPYLAPEVLEDNDYGRAVDWGLGVVYEMMCGRLPFYFNQDHEKLFEL 360  
Db 345 KDGATMTKTCGTPPYLAPEVLEDNDYGRAVDWGLGVVYEMMCGRLPFYFNQDHEKLFEL 404  
Qy 361 ILMEIIRPRTLGPPEAKSLLSGLLKOPKORLGGGSEDAKEIMQHRFPFAGIWMQHVYK 420  
Db 405 ILMEIIRPRTLGPPEAKSLLSGLLKOPKORLGGGSEDAKEIMQHRFPFAGIWMQHVYK 464  
Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYSASGTA 480  
Db 465 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYSASGTA 524

RESULT 15  
US-10-365-348-11

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; Sequence 11, Application US/10365348
; Publication No. US20040038883A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Luo, Yan
; APPLICANT: Giranda, Vincent L.
; APPLICANT: Richardson, Paul L.
; APPLICANT: Smith, Richard A.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF AKT AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 6904 US P1
; CURRENT APPLICATION NUMBER: US/10/365,348
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 10/103,256
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-365-348-11
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Query Match 99.8%; Score 2544; DB 15; Length 524;
Best Local Similarity 99.8%; Pred. No. 7.4e-165;
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLKRGVEIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNNFSVAQC 60
Db 45 MSDVAIVKEGWLKRGVEIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNNFSVAQC 104

Qy 61 QLMKTERPRNPTFIIRCLQWTVIERTFHVETPEEREETWTAIQTVADGLKKQEEEMDF 120
Db 105 QLMKTERPRNPTFIIRCLQWTVIERTFHVETPEEREETWTAIQTVADGLKKQEEEMDF 164

Qy 121 RSGSPSDNSGAEEMEVSIAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYANKI 180
Db 165 RSGSPSDNSGAEEMEVSIAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYANKI 224

Qy 181 LKKEVIVAKDVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240
Db 225 LKKEVIVAKDVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 284

Qy 241 RRVFSEDRARFYGAIEVSALDYLHSEKNVYVYRDLENLMLDKDGHIKITDFGLCKEGI 300
Db 285 RRVFSEDRARFYGAIEVSALDYLHSEKNVYVYRDLENLMLDKDGHIKITDFGLCKEGI 344

Qy 301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWNGLGVMYEMMCGRLPFYVNDHEKLFEL 360
Db 345 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWNGLGVMYEMMCGRLPFYVNDHEKLFEL 404

Qy 361 ILMEIIRPRTLGPPEAKSLGLKDPKORLGGSEDAKEIMOHRRFAGIVMOHVYEKK 420
Db 405 ILMEIIRPRTLGPPEAKSLGLKDPKORLGGSEDAKEIMOHRRFAGIVMOHVYEKK 464

Qy 421 LSPPFKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYASGTA 480
Db 465 LSPPFKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRRPHFPQFSYASSTA 524
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Search completed: February 23, 2005, 21:00:58  
Job time : 134 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: February 23, 2005, 20:23:28 ; Search time 174 Seconds  
(without alignments)  
1412.632 Million cell updates/sec

Title: US-10-621-485A-1  
Perfect score: 2550  
Sequence: 1 MSDVAIVKEGLHKGVEIK.....VDSERRPHFPQFSASGTA 480

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match | Length | ID         | Description         |
|------------|--------|-------------|--------|------------|---------------------|
| 1          | 2550   | 100.0       | 480    | Q9BWB6     | Q9BWB6 homo sapien  |
| 2          | 2544   | 99.8        | 480    | KRAC_HUMAN | P31749 homo sapien  |
| 3          | 2509   | 98.4        | 501    | KAKT_MLVAT | P31748 akt8 murine  |
| 4          | 2507   | 98.3        | 480    | KRAC_RAT   | P47196 rattus norv  |
| 5          | 2503   | 98.2        | 480    | KRAC_MOUSE | P31750 mus musculus |
| 6          | 2464   | 96.6        | 480    | O57513     | O57513 gallus gall  |
| 7          | 2452   | 96.2        | 480    | KRAC_BOVIN | Q01314 bos taurus   |
| 8          | 2378.5 | 93.3        | 481    | Q98TY9     | Q98TY9 xenopus lae  |
| 9          | 2303   | 90.3        | 452    | Q8BS26     | Q8BS26 mus musculus |
| 10         | 2128.5 | 83.5        | 481    | AKT2_MOUSE | Q60823 mus musculus |
| 11         | 2126.5 | 83.4        | 481    | AKT2_HUMAN | P31751 homo sapien  |
| 12         | 2119   | 83.1        | 486    | O72X15     | O72X15 xenopus lae  |
| 13         | 2113.5 | 82.9        | 481    | AKT2_RAT   | P47197 rattus norv  |
| 14         | 2105.5 | 82.6        | 479    | AKT3_HUMAN | Q9Y243 homo sapien  |
| 15         | 2103.5 | 82.5        | 485    | Q61P76     | Q61P76 xenopus lae  |
| 16         | 2102.5 | 82.5        | 479    | Q6NXW0     | Q6NXW0 mus musculus |
| 17         | 2097.5 | 82.3        | 479    | AKT3_MOUSE | Q9WU66 mus musculus |
| 18         | 2066.5 | 81.0        | 479    | Q8UUK0     | Q8UUK0 brachydanio  |
| 19         | 1989.5 | 78.0        | 454    | AKT3_RAT   | Q63484 rattus norv  |
| 20         | 1988   | 78.0        | 478    | Q802Y3     | Q802Y3 brachydanio  |
| 21         | 1640.5 | 64.3        | 528    | Q868D7     | Q868D7 aedes aegypt |
| 22         | 1615   | 63.3        | 571    | O7QK56     | O7QK56 anopheles g  |
| 23         | 1607.5 | 63.0        | 486    | Q95YJ0     | Q95YJ0 asterina pe  |
| 24         | 1595.5 | 62.6        | 353    | Q8CE74     | Q8CE74 mus musculus |
| 25         | 1582.5 | 62.1        | 530    | Q24293     | Q24293 drosophila   |
| 26         | 1581.5 | 62.0        | 530    | Q24469     | Q24469 drosophila   |
| 27         | 1581.5 | 62.0        | 611    | Q8INB9     | Q8INB9 drosophila   |
| 28         | 1581.5 | 62.0        | 611    | O7JN11     | O7JN11 drosophila   |
| 29         | 1490.5 | 58.5        | 546    | O17942     | O17942 caenorhabdi  |
| 30         | 1470   | 57.6        | 541    | Q17941     | Q17941 caenorhabdi  |
| 31         | 1390.5 | 54.5        | 528    | Q9XTG7     | Q9XTG7 caenorhabdi  |

|          |  |   |      |         |
|----------|--|---|------|---------|
| RESULT 1 |  |   |      |         |
| Q9BWB6   | Q9BWB6   | PRELIMINARY;                            | PRT; | 480 AA. |
| AC       | Q9BWB6;  |   |      |         |
| DT       | 01-JUN-2001  | (TrEMBLrel. 17, Created)                |      |         |
| DT       | 01-JUN-2001  | (TrEMBLrel. 17, Last sequence update)   |      |         |
| DT       | 01-OCT-2003  | (TrEMBLrel. 25, Last annotation update) |      |         |
| DE       | AKT1 protein.  |   |      |         |
| OS       | Homo sapiens (Human).  |   |      |         |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |   |      |         |
| OC       | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.   |   |      |         |
| OX       | NCBI_TaxID=9606;   |   |      |         |
| RN       | [1]  |   |      |         |
| RP       | SEQUENCE FROM N.A.   |   |      |         |
| RC       | TISSUE=Muscle;   |   |      |         |
| RX       | MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;   |   |      |         |
| RA       | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; |   |      |         |
| RT       | "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";   |   |      |         |
| RL       | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).   |   |      |         |
| RN       | [2]  |   |      |         |
| RP       | SEQUENCE FROM N.A.   |   |      |         |
| RC       | TISSUE=Muscle;   |   |      |         |
| RA       | Strausberg R.;   |   |      |         |
| RL       | Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  |   |      |         |
| CC       | -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  |   |      |         |
| CC       | -1- SIMILARITY: Contains 1 PH domain.  |   |      |         |
| DR       | EMBL; BC000479; AA00479.1; -.  |   |      |         |
| DR       | HSP; P31749; 1H10.   |   |      |         |
| DR       | GO; GO:0005524; F:ATP binding; IEA.  |   |      |         |
| DR       | GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.   |   |      |         |
| DR       | GO; GO:0016740; P:transferase activity; IEA.   |   |      |         |
| DR       | GO; GO:0006468; P:protein amino acid phosphorylation; IEA.   |   |      |         |
| DR       | InterPro; IPR011009; Kinase_like.  |   |      |         |
| DR       | InterPro; IPR001849; PH.   |   |      |         |
| DR       | InterPro; IPR011036; PH_related.   |   |      |         |
| DR       | InterPro; IPR000961; Pkinase_C.  |   |      |         |
| DR       | InterPro; IPR000719; Prot_kinase.  |   |      |         |

## ALIGNMENTS

|    |        |      |     |   |            |                    |
|----|--------|------|-----|---|------------|--------------------|
| 32 | 1324   | 51.9 | 483 | 2 | O77145     | O77145 caenorhabdi |
| 33 | 1317   | 51.6 | 387 | 2 | Q8MUAS     | Q8MUAS hydra atten |
| 34 | 1108.5 | 43.5 | 246 | 2 | Q9PUJ3     | Q9PUJ3 gallus gall |
| 35 | 1087   | 42.6 | 201 | 2 | Q9BV07     | Q9BV07 homo sapien |
| 36 | 953    | 37.4 | 286 | 2 | Q66XT6     | Q66XT6 anopheles s |
| 37 | 938    | 36.8 | 444 | 1 | KRAC_DICDI | P54644 dictyosteli |
| 38 | 901    | 35.3 | 198 | 2 | Q8C6X4     | Q8C6X4 mus musculu |
| 39 | 895    | 35.1 | 465 | 2 | O761W9     | O761W9 entamoeba h |
| 40 | 874.5  | 34.3 | 427 | 1 | SGK2_HUMAN | Q9BBY8 homo sapien |
| 41 | 862    | 33.8 | 432 | 2 | Q6U1I9     | Q6U1I9 gallus gall |
| 42 | 860.5  | 33.7 | 519 | 2 | Q6NS85     | Q6NS85 mus musculu |
| 43 | 856    | 33.6 | 687 | 2 | Q6GNZ7     | Q6GNZ7 xenopus lae |
| 44 | 855    | 33.5 | 671 | 1 | KFCB_HUMAN | P05771 homo sapien |
| 45 | 855    | 33.5 | 671 | 1 | KFCB_MOUSE | P04410 mus musculu |

```

DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TK X; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 480 AA; 55686 MW; 6EAF4F8AD436714 CRC64;

Query Match 100.0%; Score 2550; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.4e-152;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGLHKGGEYIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60
Db 1 MSDVAIVKEGLHKGGEYIKTRPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60

Qy 61 QLMKTERPRNPTFIIRCLQWTVIERTFHVETPEEREETTAIQTVADGLKKQBEEMDF 120
Db 61 QLMKTERPRNPTFIIRCLQWTVIERTFHVETPEEREETTAIQTVADGLKKQBEEMDF 120

Qy 121 RSGSPSDNSGAENEVSLAKPKHVTNNEFYLLKLGKTFGKVLVKEKATGRYYAMKI 180
Db 121 RSGSPSDNSGAENEVSLAKPKHVTNNEFYLLKLGKTFGKVLVKEKATGRYYAMKI 180

Qy 181 LKKEVIVAKDQVATLTENRVLQNSRHPFLTALXVSFQTHDRLCFVMEYANGGLFPFLHS 240
Db 181 LKKEVIVAKDQVATLTENRVLQNSRHPFLTALXVSFQTHDRLCFVMEYANGGLFPFLHS 240

Qy 241 RERFSEDRARFYGAIEVSALDYLHSEKNVYVRDLKLENLMDKGHKITDFGLCKEGI 300
Db 241 RERFSEDRARFYGAIEVSALDYLHSEKNVYVRDLKLENLMDKGHKITDFGLCKEGI 300

Qy 301 KOGATMTFCGTPYLAPEVLVDNDYGRADVWGLGVVYEMMCGRLPFYNQDHEKLFEL 360
Db 301 KOGATMTFCGTPYLAPEVLVDNDYGRADVWGLGVVYEMMCGRLPFYNQDHEKLFEL 360

Qy 361 ILMEIIRFRTLGPGLKSLGLKQPKORLGGSDAKIEMOHRFPFAGLVQHVYVEKK 420
Db 361 ILMEIIRFRTLGPGLKSLGLKQPKORLGGSDAKIEMOHRFPFAGLVQHVYVEKK 420

Qy 421 LSPFPKQVTSSETDTRYPDEFTAQMITITPPDQDDSMECVDSRRRPHFPQFSYASGTA 480
Db 421 LSPFPKQVTSSETDTRYPDEFTAQMITITPPDQDDSMECVDSRRRPHFPQFSYASGTA 480

RESULT 2
ID KRAC HUMAN STANDARD; PRT; 480 AA.
AC P31749;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE RAC-alpha serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-alpha)
DE (Protein kinase B) (PKB) (C-AKT).
GN Name=AKT1; Synonyms=PKB, RAC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91239529; PubMed=1851997;
RA Jones P.F., Jakubowicz T., Picossi F.J., Maurer F., Hemmings B.A.;
RT "Molecular cloning and identification of a serine/threonine protein
RT kinase of the second-messenger subfamily.";

```

```

RL Proc. Natl. Acad. Sci. U.S.A. 88:4171-4175(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21399046; PubMed=11508278;
RA Matsubara A., Wasson J.C., Donelan S.S., Welling C.M., Glaser B.,
RA Permutt M.A.;
RT "Isolation and characterization of the human AKT1 gene, identification
RT of 13 single nucleotide polymorphisms (SNPs), and their lack of
RT association with Type II diabetes.";
RL Diabetologia 44:910-913(2001).
RN [3]
RP SEQUENCE OF 63-480 FROM N.A.
RC TISSUE=Forebrain;
RX MEDLINE=92037600; PubMed=1718748;
RA Coffey P.J., Woodgett J.R.;
RT "Molecular cloning and characterisation of a novel putative protein-
RT serine kinase related to the cAMP-dependent and protein kinase C
RT families.";
RL Eur. J. Biochem. 201:475-481(1991).
RN [4]
RP REVISIONS.
RX MEDLINE=92249329; PubMed=1533586;
RA Coffey P.J., Woodgett J.R.;
RL Eur. J. Biochem. 205:1217-1218(1992).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=98409636; PubMed=9736715; DOI=10.1073/pnas.95.19.11211;
RA Delcommenne M., Tan C., Gray V., Rue L., Woodgett J.R., Dedhar S.;
RT "Phosphoinositide-3-OH kinase-dependent regulation of glycogen
RT synthase kinase 3 and protein kinase B/AKT by the integrin-linked
RT kinase.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:11211-11216(1998).
RN [6]
RP MUTAGENESIS OF THR-308 AND SER-473, AND PHOSPHORYLATION SITES THR-308
RP AND SER-473.
RX MEDLINE=97133284; PubMed=8978681;
RA Alessi D.R., Andjelkovic M., Caudwell F.B., Cron P., Morrice N.,
RA Cohen P., Hemmings B.A.;
RT "Mechanism of activation of protein kinase B by insulin and IGF-1.";
RL EMBO J. 15:6541-6551(1996).
RN [7]
RP PHOSPHORYLATION SITE TYR-474, AND MUTAGENESIS OF TYR-474.
RX MEDLINE=92254844; PubMed=12149249; DOI=10.1074/jbc.M203387200;
RA Conus N.M., Hannan K.M., Cristiano B.E., Hemmings B.A., Pearson R.B.;
RT "Direct identification of tyrosine 474 as a regulatory phosphorylation
RT site for the Akt protein kinase.";
RL J. Biol. Chem. 277:38021-38028(2002).
CC -I- FUNCTION: General protein kinase capable of phosphorylating
CC several known proteins.
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic and nuclear after activation by
CC integrin-linked protein kinase 1 (ILK1).
CC -I- TISSUE SPECIFICITY: In all human cell types so far analyzed
CC -I- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
CC kinase alpha (PI(3)K) results in its targeting to the plasma
CC membrane.
CC -I- PTM: Phosphorylation on Thr-308, Ser-473 and Tyr-474 is required
CC for full activity.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
CC subfamily.
CC -I- SIMILARITY: Contains 1 PH domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; M63167; AAA36539.1; -.
DR EMBL; AF283830; AAL55732.1; -.
DR EMBL; AF283819; AAL55732.1; JOINED.

```

DR EMBL; AF283820; AAL55732.1; JOINED.  
 DR EMBL; AF283821; AAL55732.1; JOINED.  
 DR EMBL; AF283822; AAL55732.1; JOINED.  
 DR EMBL; AF283823; AAL55732.1; JOINED.  
 DR EMBL; AF283824; AAL55732.1; JOINED.  
 DR EMBL; AF283825; AAL55732.1; JOINED.  
 DR EMBL; AF283826; AAL55732.1; JOINED.  
 DR EMBL; AF283827; AAL55732.1; JOINED.  
 DR EMBL; AF283828; AAL55732.1; JOINED.  
 DR EMBL; AF283829; AAL55732.1; JOINED.  
 DR EMBL; X61037; CAA43372.1; -.  
 DR PIR; A39360; A39360.  
 DR PDB; 1H10; X-ray; A=1-123.  
 DR InTact; P31749; -.  
 DR Genew; HGNC:591; AKT1.  
 DR HInvDB; HIX0012019; -.  
 DR MIM; 164730; -.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; TAS.  
 DR GO; GO:0006916; P:anti-apoptosis; TAS.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.  
 DR GO; GO:0006809; P:nitric oxide biosynthesis; TAS.  
 DR GO; GO:0006464; P:protein modification; TAS.  
 DR GO; GO:0009408; P:response to heat; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR011036; PH\_related.  
 DR InterPro; IPR000961; Pkinase\_C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase\_C; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR PROSITE; PS50003; PH DOMAIN; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW 3D-structure; ATP-binding; Nuclear protein; Phosphorylation;  
 KW Serine/threonine-protein kinase; Transferase.  
 FT DOMAIN 5 108 PH.  
 FT DOMAIN 150 408 Protein kinase.  
 FT NP\_BIND 156 164 ATP (By similarity).  
 FT BINDING 179 179 ATP (By similarity).  
 FT ACT\_SITE 274 274 Proton acceptor (By similarity).  
 FT MOD\_RES 308 308 Phosphothreonine (by PDPK1).  
 FT MOD\_RES 473 473 Phosphoserine (by ILK1).  
 FT MOD\_RES 474 474 Phosphotyrosine.  
 FT MUTAGEN 308 308 T->D: 5-fold activation and 18-fold  
 FT MUTAGEN 473 473 activation; when associated with D-473.  
 FT MUTAGEN 473 473 S->D: 7-fold activation and 25-fold  
 FT MUTAGEN 474 474 activation; when associated with D-308.  
 FT CONFLICT 173 174 Y->F: 55% inhibition of activation.  
 FT CONFLICT 202 202 L -> Q (in Ref. 3).  
 FT CONFLICT 212 212 A -> R (in Ref. 3).  
 FT CONFLICT 246 246 S -> A (in Ref. 3).  
 FT CONFLICT 409 409 A -> T (in Ref. 3).  
 FT CONFLICT 476 476 A -> P (in Ref. 3).  
 FT CONFLICT 478 478 S -> A (in Ref. 3).  
 SQ SEQUENCE 480 AA; 55716 MW; 6EAFE938AD436714 CRC64;  
 Query Match 99.8%; Score 2544; DB 1; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 3.4e-152;  
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 1 MSDVAIVKEGWLHKKGEYIKTRPRYFLKNDGTGIGYKERPDQVDQREAPLNPFVSAQC 60  
 1 MSDVAIVKEGWLHKKGEYIKTRPRYFLKNDGTGIGYKERPDQVDQREAPLNPFVSAQC 60

QY 61 QLMKTERPRNTFIIRCLQWTTVIERTPHVETPEREWTTAIQTADVADGLKKQBESEMDP 120  
 DB 61 QLMKTERPRNTFIIRCLQWTTVIERTPHVETPEREWTTAIQTADVADGLKKQBESEMDP 120  
 QY 121 RSGSPDSNGSABEVEVSLAKPKHRTVWNEFYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
 DB 121 RSGSPDSNGSABEVEVSLAKPKHRTVWNEFYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
 QY 181 LKKEVIVAKDEVAHTLTENRVQLNSRHPFLTALKYVSFQTHDRLCFVMEYANGGELFFHLS 240  
 DB 181 LKKEVIVAKDEVAHTLTENRVQLNSRHPFLTALKYVSFQTHDRLCFVMEYANGGELFFHLS 240  
 QY 241 RERVSEDRARFYGAEIVSALDYHSEKNVYVRLKLENMLDKDGHKIKITDFGLCKSGI 300  
 DB 241 RERVSEDRARFYGAEIVSALDYHSEKNVYVRLKLENMLDKDGHKIKITDFGLCKSGI 300  
 QY 301 KDGATMTKTCGTPEYLAPEVLEDNDYGRAVDWGLGVVYEMVMCGRLPFYQDHEKLFEL 360  
 DB 301 KDGATMTKTCGTPEYLAPEVLEDNDYGRAVDWGLGVVYEMVMCGRLPFYQDHEKLFEL 360  
 QY 361 ILMEIIRPRTLGPPEAKSLGSLKQDKQRLGGSGEDAKIMQHRFPFAGIVMQHVYKK 420  
 DB 361 ILMEIIRPRTLGPPEAKSLGSLKQDKQRLGGSGEDAKIMQHRFPFAGIVMQHVYKK 420  
 QY 421 LSPPFKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRPHFPQFSYASGTA 480  
 DB 421 LSPPFKQVTSSETDTRYFDEEFTAQMITITPPDODDSMECVDSERRPHFPQFSYASGTA 480

RESULT 3  
 KAKT\_MLVAT STANDARD; PRT; 501 AA.  
 AC P31748;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE AKT kinase transforming protein (EC 2.7.1.-).  
 GN Name=V-AKT;  
 OS AKT8 murine leukemia virus.  
 OC Viruses; Retroviral viruses; Retroviridae; Gammaretrovirus.  
 OX NCBI\_TaxID=11790;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92022574; PubMed=1833819;  
 RA Bellacosa A., Testa J.R., Staal S.P., Tsichlis P.N.;  
 RT "A retroviral oncogene, akt, encoding a serine-threonine kinase  
 containing an SH2-like region.";  
 RL Science 254:274-277(1991).  
 CC -!- PTM: Autophosphorylated on threonine and serine residues.  
 CC -!- MISCELLANEOUS: This protein is synthesized as a gag-Akt  
 polyprotein.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC  
 subfamily.  
 CC -!- SIMILARITY: Contains 1 PH domain.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 DR EMBL; M80675; AAA42545.1; -.  
 DR HSSP; P31749; 1H10.  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR011036; PH\_related.  
 DR InterPro; IPR000961; Pkinase\_C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.

```
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase; C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
DR ATP-binding; Oncogene; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 26 129
FT DOMAIN 171 429
FT NP_BIND 177 185
FT BINDING 200 200
FT ACT_SITE 295 295
FT MOD_RES 347 347
SQ SEQUENCE 501 AA; 57870 MW; 5AEFDE58CD42F773 CRC64;

Query Match 98.4%; Score 2509; DB 1; Length 501;
Best Local Similarity 98.3%; Pred. No. 5.7e-150;
Matches 472; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKRPQVDVDOREAPLNFSVAQC 60
Db 22 MNDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKRPQVDVDOREAPLNFSVAQC 81

Qy 61 QLMKTERPRNPTFIIRCLQWTTVIERTFHVETPEEREETWTAIQTVADGLKKQEEEMDF 120
Db 82 QLMKTERPRNPTFIIRCLQWTTVIERTFHVETPEEREETWTAIQTVADGLKKQEEEMDF 141

Qy 121 RSGSPSDNSGAEEVSLAKPKHRTVWNEPYLKLKGTFGKVLIVKEKATGRYYAMKI 180
Db 142 RSGSPSDNSGAEEVSLAKPKHRTVWNEPYLKLKGTFGKVLIVKEKATGRYYAMKI 201

Qy 181 LKKEVIVAKDVAHTLFTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240
Db 202 LKKEVIVAKDVAHTLFTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 261

Qy 241 RERFVEDRFRFYGAIEVSALDYLHSEKNVYVRDLKLENLMDKXGHIKITDFGLCKEGI 300
Db 262 RERFVEDRFRFYGAIEVSALDYLHSEKNVYVRDLKLENLMDKXGHIKITDFGLCKEGI 321

Qy 301 KOGATMTKTCFTPEYLAPEVLEDNDYGRAVDWGLGVVMYEMWCGRLPFYVQDHEKLFEL 360
Db 322 KOGATMTKTCFTPEYLAPEVLEDNDYGRAVDWGLGVVMYEMWCGRLPFYVQDHEKLFEL 381

Qy 361 ILMEIIRFPRTLGLPEAKSLLSGLLKXDPKQRLGGSGSDAKEIMQHRFFAGIVWQHVYEKK 420
Db 382 ILMEIIRFPRTLGLPEAKSLLSGLLKXDPQRLGGSGSDAKEIMQHRFFANIVQDVYEKK 441

Qy 421 LSPFPKQVTSSETDTRVDFEFTAQMITITPPDQDDSMCEVDSRRRPHFPQFSYASGTA 480
Db 442 LSPFPKQVTSSETDTRVDFEFTAQMITITPPDQDDSMCEVDSRRRPHFPQFSYASGTA 501
```

## RESULT 4

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KRAC RAT STANDARD; PRT; 480 AA.
AC P47196;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE RAC-alpha serine/threonine-protein kinase (EC 2.7.1.37) (RAC-pk-alpha)
DE (Protein kinase B) (PKB).
GN Name=Akt1;
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxid=10116;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RC MEDLINE=95091823; PubMed=7999118;
RA Konishi H., Shinomura T., Kuroda S.I., Ono Y., Kikkawa U.;
RT "Molecular cloning of rat RAC protein kinase alpha and beta and their
RL Biochem. Biophys. Res. Commun. 205:817-825(1994).
CC -1- FUNCTION: General protein kinase capable of phosphorylating
CC several known proteins.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear after activation by
CC integrin-linked protein kinase 1 (ILK1) (By similarity).
CC -1- TISSUE SPECIFICITY: Widely expressed. Low levels found in liver
CC with slightly higher levels present in thymus and testis.
CC -1- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
CC kinase alpha (PI(3)K) results in its targeting to the plasma
CC membrane.
CC -1- PTM: Phosphorylation on Thr-308, Ser-473 and Tyr-474 is required
CC for full activity.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
CC subfamily.
CC -1- SIMILARITY: Contains 1 PH domain.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC
CC EMBL: D30040; BAA06279.1; -.
DR PIR: JC2437; JC2437.
DR HSP; P31749; IH10.
DR RGD; 2081; Akt1.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR011849; PH.
DR InterPro; IPR011036; PH related.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase; C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferase.
FT DOMAIN 5 108
FT DOMAIN 150 408
FT NP_BIND 156 164
FT BINDING 179 179
FT ACT_SITE 274 274
FT MOD_RES 308 308
FT MOD_RES 473 473
FT MOD_RES 474 474
SQ SEQUENCE 480 AA; 55735 MW; 5DCAAE713436D04 CRC64;

Query Match 98.3%; Score 2507; DB 1; Length 480;
Best Local Similarity 98.1%; Pred. No. 7.3e-150;
Matches 471; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKRPQVDVDOREAPLNFSVAQC 60
Db 1 MNDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKRPQVDVDOREAPLNFSVAQC 60
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QY 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEREETWTAIQTVADGLKKQBEEMDF 120  
 Db 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEREETWTAIQTVADGLKKQBEEMDF 120  
 QY 121 RSGSPSDNSGAEEMVSLAKPKHRTVMNEFEYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
 Db 121 RSGSPSDNSGAEEMVSLAKPKHRTVMNEFEYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
 QY 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
 Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
 QY 241 RERVSEDRARFYGAEIVSALDYLHSEKNVYRDLEKLENMLDKDGHKIKITDFGLCKEGI 300  
 Db 241 RERVSEDRARFYGAEIVSALDYLHSEKNVYRDLEKLENMLDKDGHKIKITDFGLCKEGI 300  
 QY 301 KDGAATMTKFCGTPEYLAPEVLEDNDYGRAVDWGLGVVYEMWCGRLPFYQNDHEKLEL 360  
 Db 301 KDGAATMTKFCGTPEYLAPEVLEDNDYGRAVDWGLGVVYEMWCGRLPFYQNDHEKLEL 360  
 QY 361 ILMBEIRPRTLPKPAKSLGSLKPKQRLGGGSDAKETIMQHRFFAGIVWQHVYK 420  
 Db 361 ILMBEIRPRTLPKPAKSLGSLKPKQRLGGGSDAKETIMQHRFFAGIVWQHVYK 420  
 QY 421 LSPPEKPOVTSFTDTRYDEEFTAQMITITPPDQDSMECVDSRRPFPQFSYASGTA 480  
 Db 421 LSPPEKPOVTSFTDTRYDEEFTAQMITITPPDQDSMECVDSRRPFPQFSYASGTA 480

## RESULT 5

KRAC\_MOUSE STANDARD; PRT; 480 AA.  
 AC F31750; Q62274;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE RAC-alpha serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-alpha)  
 DE (AKT1 kinase) (Protein kinase B) (PKB) (C-AKT) (Thymoma viral proto-oncogene).  
 DE oncogene).  
 GN Name=Akt1; Synonyms=Akt, Rac;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_taxid=10090;  
 RN [1]  
 RP Bousquets X., Powell C.;  
 RL Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RC STRAIN=AKR/J; TISSUE=Thymus;  
 RX MEDLINE=93173519; PubMed=8437858;  
 RA Bellacosa A., Franke T.F., Gonzalez-Portal M.E., Datta K., Taguchi T.,  
 RA Gardner J., Cheng J.Q., Testa J.R., Teichlis P.N.;  
 RT "Structure, expression and chromosomal mapping of c-akt: relationship  
 RT to v-akt and its implications";  
 RL Oncogene 8:745-754(1993).  
 CC -!- FUNCTION: General protein kinase capable of phosphorylating  
 CC several known proteins.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear after activation by  
 CC integrin-linked protein kinase 1 (ILK1) (By similarity).  
 CC -!- TISSUE SPECIFICITY: Widely expressed. Low levels found in liver  
 CC with slightly higher levels expressed in thymus and testis.  
 CC -!- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-  
 CC kinase alpha (PI(3)K) results in its targeting to the plasma  
 CC membrane.  
 CC -!- PTM: Phosphorylation on Thr-308, Ser-473 and Tyr-474 is required  
 CC for full activity.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 1 PH domain.

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 CC -----  
 DR EMBL; M94335; AAA18254.1; -;  
 DR EMBL; X65687; CAA46620.1; -;  
 DR PIR; S33364; S33364.  
 DR HSSP; P31749; 1H10.  
 DR MGD; MGI:87986; Akt1.  
 DR GO; GO:0005737; C:cytoplasm; IDA.  
 DR GO; GO:0005515; P:protein binding; IPI.  
 DR GO; GO:0006915; P:apoptosis; IDA.  
 DR GO; GO:0008637; P:apoptotic mitochondrial changes; IDA.  
 DR GO; GO:0007281; P:germ-cell development; IDA.  
 DR GO; GO:0006488; P:protein amino acid phosphorylation; IDA.  
 DR GO; GO:0030163; P:protein catabolism; IDA.  
 DR GO; GO:0016567; P:protein ubiquitination; IDA.  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR011036; PH related.  
 DR InterPro; IPR000961; PKinase\_C.  
 DR InterPro; IPR000719; Prot\_Kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase\_C; 1.  
 DR ProDom; PD000001; Prot\_Kinase; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR PROSITE; PS50003; PH DOMAIN; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS0108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;  
 KW Transferase.  
 KW DOMAIN 5 108 PH.  
 FT DOMAIN 150 408 Protein kinase.  
 FT NP\_BIND 156 164 ATP (By similarity).  
 FT BINDING 179 179 ATP (By similarity).  
 FT ACT\_SITE 274 274 Proton acceptor (By similarity).  
 FT MOD\_RES 308 308 Phosphothreonine (by PDPK1) (By  
 FT similarity).  
 FT MOD\_RES 473 473 Phosphoserine (by ILK1) (By similarity).  
 FT MOD\_RES 474 474 Phosphotyrosine (By similarity).  
 FT CONFLICT 367 367 A -> R (in Ref. 2).  
 SQ SEQUENCE 480 AA; 55622 MW; 18D21018593B5A98 CRC64;  
 Query Match 98.2%; Score 2503; DB 1; Length 480;  
 Best Local Similarity 98.1%; Pred. No. 1.3e-149;  
 Matches 471; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 MSDVAIVKEGWLHKRGYIKTWPRYFLKNDGTFYGYKERPDVDQREAPLNFSVAQC 60  
 Db 1 MNDVAIVKEGWLHKRGYIKTWPRYFLKNDGTFYGYKERPDVDQREAPLNFSVAQC 60  
 QY 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEREETWTAIQTVADGLKKQBEEMDF 120  
 Db 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEREETWTAIQTVADGLKKQBEEMDF 120  
 QY 121 RSGSPSDNSGAEEMVSLAKPKHRTVMNEFEYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
 Db 121 RSGSPSDNSGAEEMVSLAKPKHRTVMNEFEYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
 QY 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
 Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240

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Qy 241 RRVFSDRFRFYGAIEVSALDYHSEKNVYVRDLKLENLMLDKDGHIKITDFGLCKEGI 300
Db 241 RRVFSDRFRFYGAIEVSALDYHSEKNVYVRDLKLENLMLDKDGHIKITDFGLCKEGI 300
Qy 301 KDGATMKTFCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360
Db 301 KDGATMKTFCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360
Qy 361 ILMEIEIRPRTLGPPEAKSLLSGLLKDPKQRLGGGSEDAKEIMQHRFFAGIIVQHVYVEKK 420
Db 361 ILMEIEIRPRTLGPPEAKSLLSGLLKDPKQRLGGGSEDAKEIMQHRFFAGIIVQHVYVEKK 420
Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480
Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480

RESULT 6
O57513 PRELIMINARY; PRT; 480 AA.
AC O57513
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serine/threonine protein kinase.
GN Name=akt1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Theelen M., Swinkels S.U.M., de Jong M.D.M., Thomas A.A.M.,
RA Verkley A.J., Hanafusa H., Hummel B.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL; AF039943; AAB94767.1; -.
DR HSSP; P31749; IHI0.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH related.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 480 AA; 55723 MW; 3883A47PD6689626 CRC64;

Query Match
Best Local Similarity 96.6%; Score 2464; DB 2; Length 480;
Matches 461; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MSDAIVKEGHLHKGVEIKTWRRPYFLKNDGTFIGYKERPDQVDQREAPLNFSVAQC 60
Db 1 MNEVAIVKEGHLHKGVEIKTWRRPYFLKNDGTFIGYKERPDQVDQREAPLNFSVAQC 60

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Qy 61 QLMKTERPRNTFIIRCLQMTTIVERTFHVETPEEREEMTTAQTQVADGLKKQEEEMDF 120
Db 61 QLMKTERPKNTFIIRCLQMTTIVERTFHVETPEEREEMTTAQTQVADSLKKQEEEMDF 120
Qy 121 RSGSPSDNSGAEMEVSALAKPKHRVTWMEFEYILKLKGTFGKVILVKEKATGRYYAMKI 180
Db 121 RSGSPSDNSGAEMEVSMTKPKHVTWMEFEYILKLKGTFGKVILVKEKATGRYYAMKI 180
Qy 181 LKKEVIVAKDEVATHLTENRVLQNSRHPFLTALKYSPQTHDRLCFVMEYANGGELFPHLS 240
Db 181 LKKEVIVAKDEVATHLTENRVLQNSRHPFLTALKYSPQTHDRLCFVMEYANGGELFPHLS 240
Qy 241 RRVFSDRFRFYGAIEVSALDYHSEKNVYVRDLKLENLMLDKDGHIKITDFGLCKEGI 300
Db 241 RRVFSDRFRFYGAIEVSALDYHSEKNVYVRDLKLENLMLDKDGHIKITDFGLCKEGI 300
Qy 301 KDGATMKTFCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360
Db 301 KDGATMKTFCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360
Qy 361 ILMEIEIRPRTLGPPEAKSLLSGLLKDPKQRLGGGSEDAKEIMQHRFFAGIIVQHVYVEKK 420
Db 361 ILMEIEIRPRTLGPPEAKSLLSGLLKDPKQRLGGGSEDAKEIMQHRFFAGIIVQHVYVEKK 420
Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480
Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYSASGTA 480

RESULT 7
KRAC_BOVIN
ID KRAC_BOVIN STANDARD; PRT; 480 AA.
AC Q01314;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE RAC-alpha serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-alpha)
DE (Protein kinase B) (PKB).
GN Name=AKT1; Synonyms=PKB;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92037600; PubMed=1718748;
RA Coffey P.J., Woodgett J.R.;
RT "Molecular cloning and characterisation of a novel putative protein-
RT serine kinase related to the CAMP-dependent and protein kinase C
RT families."
RL Eur. J. Biochem. 201:475-481(1991).
RN [2]
RP REVISIONS.
RX MEDLINE=9249329; PubMed=1533586;
RA Coffey P.J., Woodgett J.R.;
RL Eur. J. Biochem. 205:1217-1218(1992).
CC -1- FUNCTION: General protein kinase capable of phosphorylating
CC several known proteins.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear after activation by
CC integrin-linked protein kinase 1 (ILK).
CC -1- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
CC kinase alpha (PI(3)K) results in its targeting to the plasma
CC membrane.
CC -1- PTM: Phosphorylation on Thr-308, Ser-473 and Tyr-474 is required
CC for full activity.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
CC subfamily.
CC -1- SIMILARITY: Contains 1 PH domain.

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 DR EMBL; X61036; CAM43371.1; -;  
 DR PIR; S62117; S62117.  
 DR HSSP; P31749; 1H10.  
 DR InterAct; Q01314; -;  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR001849; PH\_related.  
 DR InterPro; IPR011036; PH\_related.  
 DR InterPro; IPR000961; Pkinase\_C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase\_C; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE; PS00003; PH\_DOMAIN; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR ATP-binding; Phosphorylation; Serine/threonine-protein kinase;  
 KW Transferase.  
 FT DOMAIN 5 108 PH.  
 FT NP\_BIND 150 408 Protein kinase.  
 FT BINDING 156 164 ATP (By similarity).  
 FT ACT\_SITE 274 274 Proton acceptor (By similarity).  
 FT MOD\_RES 308 308 Phosphothreonine (by PDK1).  
 FT MOD\_RES 473 473 Phosphoserine (by ILK1).  
 FT MOD\_RES 474 474 Phosphotyrosine (By similarity).  
 SQ SEQUENCE 480 AA; 55617 MW; 0BAC4123ED5A848 CRC64;

Query Match 96.2%; Score 2452; DB 1; Length 480;  
 Best Local Similarity 96.2%; Pred. No. 2.1e-146; Mismatches 11; Indels 0; Gaps 0;  
 Matches 462; Conservative 7;

Qy 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKERPDQVQDQREAPLNFSVAQC 60  
 Db 1 MNDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKERPDQVQDQREAPLNFSVAQC 60  
 Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTPHVETPEREETWTAIQTVADGLKQEEEMDF 120  
 Db 61 QLMKTERPRNTFIIRCLQWTTVIERTPHVETPEREETWTAIQTVADGLKQEEEMDF 120  
 Qy 121 RSGSPDNGSGAEEMVSLAKPKHRTVMNEFEYLLKLGKGTGKVLVKEKATGRYAMK 180  
 Db 121 RSGSPDNGSGAEEMVSLAKPKHRTVMNEFEYLLKLGKGTGKVLVKEKATGRYAMK 180  
 Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
 Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
 Qy 241 RERVFSDEDRARFYGAEIVSALDYHSEKQNVYRDLKLENLMDKDGHIKITDFGLCKEGI 300  
 Db 241 RERVFSDEDRARFYGAEIVSALDYHSEKQNVYRDLKLENLMDKDGHIKITDFGLCKEGI 300  
 Qy 301 KDGATMTKTCCTPEYLAPEVLNDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
 Db 301 KDGATMTKTCCTPEYLAPEVLNDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
 Qy 361 ILMEIIRPRTLPGPEAKSLLSGLLKDPKQRLGGSEDAKSIQHRFPAGIIVQHWYVEKK 420  
 Db 361 ILMEIIRPRTLPGPEAKSLLSGLLKDPKQRLGGSEDAKSIQHRFPAGIIVQHWYVEKK 420

Qy 421 LSPFPKQVTSSETDTRFYDEFTTAQMITTPPDQDSDMECVDSRRRPHFPQFSASGTA 480  
 Db 421 LSPFPKQVTSSETDTRFYDEFTTAQMITTPPDQDSDMEGVDSRRRPHFPQFSASATA 480

## RESULT 8

Q98TY9 PRELIMINARY; PRT; 481 AA.  
 AC Q98TY9  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Akt.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Andersen C.B., Sakae H., Roth R.A., Conti M.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC -1- SIMILARITY: Contains 1 PH domain.  
 DR EMBL; AF317656; AAC59601.1; -;  
 DR HSSP; P31751; IMRY.  
 DR GO; GO:000524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR011036; PH\_related.  
 DR InterPro; IPR000961; Pkinase\_C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase\_C; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR PROSITE; PS00003; PH\_DOMAIN; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 481 AA; 56042 MW; FF56CFB9A6454303 CRC64;

Query Match 93.3%; Score 2378.5; DB 2; Length 481;  
 Best Local Similarity 93.1%; Pred. No. 9e-142;  
 Matches 448; Conservative 15; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKERPDQVQDQREAPLNFSVAQC 60  
 Db 1 MNEVAIVKEGWLHKGRIYKTRPRYFLKSDGTFIGYKERPDQVQDQLETPLNFSVAKC 60  
 Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTPHVETPEREETWTAIQTVADGLKQEEEMDF 120  
 Db 61 QLMKTERPKNTFIIRCLQWTTVIERTPHVDSPEEREETWTAIQTVADNLDKQEEEMEV 120  
 Qy 121 RSG-SPSDNGSGAEEMVSLAKPKHRTVMNEFEYLLKLGKGTGKVLVKEKATGRYAMK 179  
 Db 121 RSGSDPSDNGSGAEEMVSHSKPKHRTVMNEFEYLLKLGKGTGKVLVKEKATGRYAMK 180  
 Qy 180 ILKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHL 239  
 Db 181 ILKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHL 240  
 Qy 240 SRRVFSDEDRARFYGAEIVSALDYHSEKQNVYRDLKLENLMDKDGHIKITDFGLCKEG 299

Db 241 SRERIFSEDARFYCAETVSALDYLHSEKNVYVRDLKLENLMLDKGHKITDPLGCKEG 300  
 Qy 300 IKDQATWKTFCGTPEYLAPEVLENDYGRAVDWGLGVVWYEMWCGRLPFVNDQHEKLF 359  
 Db 301 IKDQATWKTFCGTPEYLAPEVLENDYGRAVDWGLGVVWYEMWCGRLPFVNDQHEKLF 360  
 Qy 360 LILMEEIRFPRTLGLPEAKSLSLGLKKDKPKQRLGGSGSEDAKEIMQHRFFAGIVMQRHYVEK 419  
 Db 361 LILMEEIRFPRTLGLPEAKSLSLGLKKDKPKQRLGGSGPDDAKEIMQHRFFAGIVMQRHYVEK 420  
 Qy 420 KLSPPFPQVTSQTDTRYFDBEFTQAQMTITPPQDDSMCEVCDSRERPHFPQSYSASGT 479  
 Db 421 KLVPFPQVTSQTDTRYFDBEFTQAQMTITPPQDDNFVNDNERPHFPQSYSASGN 480  
 Qy 480 A 480  
 Db 481 A 481

RESULT 9  
 Q8BS26 PRELIMINARY; PRT; 452 AA.  
 ID Q8BS26; AC Q8BS26; DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Mus musculus adult male aorta and vein cDNA, RIKEN full-length  
 DE enriched library, clone:A330023F15 product:thymoma viral proto-  
 DE oncogene 1, full insert sequence.  
 GN Name=Akti;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RX Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning."  
 RL Mech. Enzymol. 303:19-44 (1999).  
 RN [2]  
 RP STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RX RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690 (2001).  
 RN [3]  
 RP STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
 RC The FANTOM Consortium;  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs."  
 RL Nature 420:563-573 (2002).  
 RN [4]  
 RP STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RX Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes."  
 RL Genome Res. 10:1617-1630 (2000).  
 RN [5]  
 RP STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 Fujiwaka S., Inoue K., Togawa Y., Tanaka M., Ohara E., Watahiki M.,  
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771 (2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akai S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC -1- SIMILARITY: Contains 1 PH domain.  
 DR EMBL; AK040758; BAC30695.1; -.  
 DR HSSP; P31749; 1H10.  
 DR MGD; MGI:87986; Akt1.  
 DR GO; GO:0005737; Cytoplasm; IDA.  
 DR GO; GO:0030027; Cilamellipodium; IDA.  
 DR GO; GO:0005515; F-protein binding; IPI.  
 DR GO; GO:0004672; F-protein kinase activity; IDA.  
 DR GO; GO:0006915; P:apoptosis; IDA.  
 DR GO; GO:0008637; P:apoptotic mitochondrial changes; IDA.  
 DR GO; GO:0007281; P:germ cell development; IDA.  
 DR GO; GO:0043066; P:negative regulation of apoptosis; IDA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.  
 DR GO; GO:0003163; P:protein catabolism; IDA.  
 DR GO; GO:0016567; P:protein ubiquitination; IDA.  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR011036; PH-related.  
 DR InterPro; IPR000961; Pkinase\_C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00089; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase\_C; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR SMART; SM00133; S\_TKc; 1.  
 DR PROSITE; PS00003; PH\_DOMAIN; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 452 AA; 52618 MW; E203C8F46A18E5E CRC64;  
 Query Match 90.3%; Score 2303; DB 2; Length 452;  
 Best Local Similarity 98.0%; Pred. No. 4.8e-137;  
 Matches 433; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 MSDVAIVKCGWLHRCGEYIKTWPRVFLKNDCTFGYKERPDVDQREAPLNFSVAQC 60  
 Db 1 MNDVAIVKCGWLHRCGEYIKTWPRVFLKNDCTFGYKERPDVDQREAPLNFSVAQC 60  
 Qy 61 QLMKTERPRENTFIIRCLQWTTVIERTFHVETPEEREETWTATQTVDGLKKQEEEMDF 120  
 Db 61 QLMKTERPRENTFIIRCLQWTTVIERTFHVETPEEREETWTATQTVDGLKKQEEEMDF 120  
 Qy 121 RSGSPDNGSABEMEVSLAKPKHRVTWNEPEYIKLJGKGTFGKVLVKEKATGRYYANKI 180



Db 121 RSGSPSDNSGAEEMVSLAKPKHRTVMNEPEVYLKLGKGTGKVLVKEKATGRYYAMKI 180  
Qy 181 LKKEVIVAKDEVAHTLTNRVQLNSRHPFLTALKYSFQTHDRLCFVMEYANGBELFPHLS 240  
Db 181 LKKEVIVAKDEVAHTLTNRVQLNSRHPFLTALKYSFQTHDRLCFVMEYANGBELFPHLS 240  
Qy 241 RERFSEDRARFYGAIEVSALDYHSEKXNVVYRDLEKLEMLDKDGHKIKITDFGLCKEGI 300  
Db 241 RERFSEDRARFYGAIEVSALDYHSEKXNVVYRDLEKLEMLDKDGHKIKITDFGLCKEGI 300  
Qy 301 KDGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMVCGRLPFYVQDHEKLPFEL 360  
Db 301 KDGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMVCGRLPFYVQDHEKLPFEL 360  
Qy 361 ILMEIRPPRTLGPEAKSLLSGLLKQDPKQRLGGSGEDAKIMQHRFPAGIYVQHVYKK 420  
Db 361 ILMEIRPPRTLGPEAKSLLSGLLKQDPKQRLGGSGEDAKIMQHRFPAGIYVQHVYKK 420  
Qy 421 LSPFPKPOVTSETDTRYDEDF 442  
Db 421 LSPFPKPOVTSETDTRYDEDF 442

RESULT 10  
AKT2 MOUSE  
ID AKT2 MOUSE STANDARD; PRT; 481 AA.  
AC Q60823;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE RAC-beta serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-beta)  
DE (Protein kinase Akt-2) (Protein kinase B, beta) (PKB beta).  
GN Name=Akt2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;  
RX MEDLINE=96032568; PubMed=7566964;  
RA Altomare D.A., Guo K., Cheng J.Q., Sonoda G., Waleh K., Testa J.R.;  
RT "Cloning, chromosomal localization and expression analysis of the  
RT mouse Akt2 oncogene.";  
RL Oncogene 11:1055-1060(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Retina, and Salivary gland;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh P.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fanev J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: General protein kinase capable of phosphorylating  
CC several known proteins  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC

CC subfamily.  
CC -!- SIMILARITY: Contains 1 PH domain.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; U22445; AAA3557.1; --  
CC EMBL; BC026151; AAH26151.1; --  
CC EMBL; BC040377; AAH40377.1; --  
CC HSP; P31751; IGZK.  
CC MGD; MGI:104874; Akt2.  
CC InterPro; IPR011009; Kinase\_like.  
CC InterPro; IPR011036; PH related.  
CC InterPro; IPR011849; PH.  
CC InterPro; IPR000961; Kinase\_C.  
CC InterPro; IPR000719; Prot\_kinase.  
CC InterPro; IPR008271; Ser\_thr\_kin\_AS.  
CC Pfam; PF00169; PH; 1.  
CC Pfam; PF00069; Pkinase; 1.  
CC Pfam; PF00433; Pkinase\_C; 1.  
CC ProDom; PD000001; Prot\_kinase; 1.  
CC PROSITE; PS00003; PH DOMAIN; 1.  
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
CC PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
CC PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
CC ATP-binding; Serine/threonine-protein kinase; Transferase.  
CC DOMAIN 5 108 PH.  
CC FT DOMAIN 152 409. Protein kinase.  
CC FT NP\_BIND 158 166 ATP (By similarity).  
CC FT BINDING 181 181 ATP (By similarity).  
CC FT ACT\_SITE 275 275 Proton acceptor (By similarity).  
CC SQ SEQUENCE 481 AA; 55741 MW; 4AB4A9C4FB9CEA7D CRC64;  
  
Query Match 83.5%; Score 2128.5; DB 1; Length 481;  
Best Local Similarity 81.8%; Pred. No. 5e-126;  
Matches 392; Conservative 52; Mismatches 32; Indels 3; Gaps 2;  
  
Qy 1 MSDVAIVKEGWLHKGKGVYKTRPRYFLKNDGTGFIGYKERPDQVDQREAPLNPSVAQC 60  
Db 1 MNEVSVIKBGLHKGKGVYKTRPRYFLKSDGSGFIGYKERPEAPDQTLPLNPSVAEC 60  
  
Qy 61 QLMKTERPRNTFIIRCLQMTVTIERTPHVETPEREETWTTAIQTVDGLKKQ--EEEM 118  
Db 61 QLMKTERPRNTFVIRCLQMTVTIERTPHVDSPEREEMWRAIQVANSLSKQRGEDAM 120  
  
Qy 119 DFRSGSPSDNSGAEEMVSLAKPKHRTVMNEPEVYLKLGKGTGKVLVKEKATGRYYAM 178  
Db 121 DYKCGSPSDSSTSEMEVAVNKAARAKVTMNDFDYLLKLGKGTGKVLVKEKATGRYYAM 180  
  
Qy 179 KILKEVIVAKDEVAHTLTNRVQLNSRHPFLTALKYSFQTHDRLCFVMEYANGBELFPH 238  
Db 181 KILKEVIVAKDEVAHTLTNRVQLNSRHPFLTALKYSFQTHDRLCFVMEYANGBELFPH 240  
  
Qy 239 LSRRVSEDRARFYGAIEVSALDYHSEKXNVVYRDLEKLEMLDKDGHKIKITDFGLCKE 298  
Db 241 LSRRVSEDRARFYGAIEVSALDYHSEKXNVVYRDLEKLEMLDKDGHKIKITDFGLCKE 299  
  
Qy 299 GIKDGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMVCGRLPFYVQDHEKLP 358  
Db 300 GISDGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMVCGRLPFYVQDHEKLP 359  
  
Qy 359 ELIIMEIRPPRTLGPEAKSLLSGLLKQDPKQRLGGSGEDAKIMQHRFPAGIYVQHVY 418  
Db 360 ELIIMEIRPPRTLGPEAKSLLSGLLKQDPKQRLGGSGEDAKIMQHRFPAGIYVQHVY 419  
  
Qy 419 KKLSPFPKPOVTSETDTRYDEEFTAQMITTPPDQDSDMECVDSERPHPPQPSYSAS 477  
Db 420 KKLSPFPKPOVTSETDTRYDEEFTAQMITTPPDQDSDMECVDSERPHPPQPSYSAS 478

RESULT 11  
 ID AKT2\_HUMAN STANDARD; PRT; 481 AA.  
 AC P31751.  
 DT 01-JUN-1993 (Rel. 26, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE RAC-beta serine/threonine-protein kinase (SC 2.7.1.37) (RAC-PK-beta)  
 DE (Protein kinase Akt-2) (Protein kinase B, beta) (PKB beta).  
 GN Name=Akt2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Epithelium;  
 RX MEDLINE=9219887; PubMed=1801921;  
 RA Jones P.F., Jakubowicz T., Hemmings B.A.;  
 RT "Molecular cloning of a second form of rac protein kinase.";  
 RL Cell Regul. 2:1001-1009(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Cheng J.Q., Godwin A.K., Bellacosa A., Taguchi T., Franke T.F.,  
 RA Hamilton T.C., Teichlis P.N., Testa J.R.;  
 RT "AKT2, a putative oncogene encoding a member of a subfamily of  
 RT protein-serine/threonine kinases, is amplified in human ovarian  
 RT carcinomas";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:9267-9271(1992).  
 CC -1- FUNCTION: General protein kinase capable of phosphorylating  
 CC several known proteins.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- TISSUE SPECIFICITY: In all human cell types so far analyzed.  
 CC -1- DISEASE: Alterations of AKT2 may contribute to the pathogenesis of  
 CC ovarian carcinomas.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC  
 CC subfamily.  
 CC -1- SIMILARITY: Contains 1 PH domain.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; M77198; AAA36585.1; -.  
 CC EMBL; M95936; AAA58364.1; -.  
 CC PIR; A46288; A46288.  
 CC PDB; 1GZK; X-ray; A=146-459.  
 CC PDB; 1GZN; X-ray; A=146-480.  
 CC PDB; 1GZO; X-ray; A=146-459.  
 CC PDB; 1MRV; X-ray; A=143-481.  
 CC PDB; 1MRV; X-ray; A=143-481.  
 CC InAct; P31751; -.  
 CC Genew; HGNC:392; AKT2.  
 CC MIM; 164731; -.  
 CC GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.  
 CC GO; GO:0006464; P:protein modification; TAS.  
 CC InterPro; IPR011009; Kinase\_like.  
 CC InterPro; IPR001849; PH.  
 CC InterPro; IPR011036; PH\_related.  
 CC InterPro; IPR000961; Pkinase\_C.  
 CC InterPro; IPR000719; Prot\_kinase.  
 CC InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 CC InterPro; IPR002290; Ser\_thr\_kinase.  
 CC Pfam; PF00169; PH; 1.  
 CC Pfam; PF00069; Pkinase; 1.  
 CC Pfam; PF00433; Pkinase\_C; 1.

DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SMO0233; PH; 1.  
 DR SMART; SMO0133; S\_TK\_X; 1.  
 DR SMART; SMO0220; S\_TKC; 1.  
 DR PROSITE; PS50003; PH DOMAIN; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.  
 KW 3D-structure; ATP-binding; Serine/threonine-protein kinase;  
 KW Transferase.  
 FT DOMAIN 5 108 PH.  
 FT DOMAIN 152 409 Protein kinase.  
 FT NP\_BIND 158 166 ATP (By similarity).  
 FT BINDING 181 181 ATP (By similarity).  
 FT ACT\_SITE 275 275 Proton acceptor (By similarity).  
 FT CONFLICT 478 481 SIRE -> PREEKDLMLFVSLPDLPSDFSLKSHSPSSNF  
 FT ILLSFSLKK (in Ref. 1)  
 SQ SEQUENCE 481 AA; 55768 MW; B18C87A7246FB24 CRC64;  
 Query Match 83.4%; Score 2126.5; DB 1; Length 481;  
 Best Local Similarity 81.6%; Pred. No. 6.7e-126;  
 Matches 391; Conservative 52; Mismatches 33; Indels 3; Gaps 2;  
 Qy 1 MSDVAIVKEGWLHKGREYIKTWPRPYLLKNDGTFYKRPDPVDVOREAPLNFSVAQC 60  
 Db 1 MNEVSVIKEGWLHKGREYIKTWPRPYLLKSDGSFYKRPDPDTLPPLNFSVAEC 60  
 Qy 61 QLMKTERPRNTFIIRCLQWTVIERTFHVETPEEREETTAIQTVADGLKKOE--EEM 118  
 Db 61 QLMKTERPRNTFVIRCLQWTVIERTFHVDSFDEREENWRAIQMVANSUKQAPGEDPM 120  
 Qy 119 DFRSGSPSDNSGAEMEVSLLAKPKRVTMNEFEYLKLLGKGTGFKVILVKEKATGRYYAM 178  
 Db 121 DYKGSFSDSDSTTEEMEVAVSKAKVWMDFDYLLGLGKGTGFKVILVREKATGRYYAM 180  
 Qy 179 KILKKEVIVAKDVAHTLTENRVLQNSRHPFLTALKYSPFOTHRDLCFVMEYANGGELFFH 238  
 Db 181 KILKKEVITAKDVAHTVTESRVLQNRHPFLTALKYAFQTHDLRCFVMEYANGGELFFH 240  
 Qy 239 LSRERFVEDRARFYGAIEVSALDYHSEKNVYVRLKLENMLDKDGHKIKITDFGLCKE 298  
 Db 241 LSRERFTEERARFYGAIEVSALDYHLS-RDVTYRDLKLENMLDKDGHKIKITDFGLCKE 299  
 Qy 299 GIKDGATMTKTCGTPPEYLAPEVLEDNDYGRAVDWGLGVVYEMWCGRLPFYNQDHEKLF 358  
 Db 300 GISDGATMTKTCGTPPEYLAPEVLEDNDYGRAVDWGLGVVYEMWCGRLPFYNQDHERLF 359  
 Qy 359 ELILMBEIRPRTLGPPEAKSLLSGLLKDPKQLGGSEDAKEIMQHRFPAGIVQHWYVE 418  
 Db 360 ELILMBEIRPRTLSPPEAKSLLAGLLKDPKQLGGGSDAKEVMEHRFFLSINWQDVVQ 419  
 Qy 419 KKLSPPKPQVTSSTTRVDEEFTAQMITITPPDODDSMECVDSERRRHPQFSYSAS 477  
 Db 420 KKLPPPKPQVTSSEVDTRYPDDEFTAQSIITPPDRYDSLGLLELDQRTTHFPQFSYSAS 478  
 RESULT 12  
 Q7ZX15  
 ID Q7ZX15 PRELIMINARY; PRT; 486 AA.  
 AC Q7ZX15;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Akt2-prov protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;



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DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH related.
DR InterPro; IPR000961; PKinase C.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; PKinase; 1.
DR Pfam; PF00433; PKinase C; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS0011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 5 108
FT DOMAIN 152 409
FT NP_BIND 158 166 ATP (By similarity).
FT BINDING 181 181 ATP (By similarity).
FT ACT_SITE 275 275 Proton acceptor (by similarity).
SQ SEQUENCE 481 AA; 55343 MW; 3C4BB65B2F376F85 CRC64;

Query Match      82.9%; Score 2113.5; DB 1; Length 481;
Best Local Similarity 81.4%; Pred. No. 4.4e-125;
Matches 390; Conservative 52; Mismatches 34; Indels 3; Gaps 2;

Qy 1 MSQVAIVKEGWLHKGVEYIKTRPRYFLLLKNDGTFIGYKRPQVDQREAPLNFSVAQC 60
Db 1 MNEYSVIEKEGWLHKGVEYIKTRPRYFLLLKSDGTFIGYKRPQVDQREAPLNFSVAEC 60

Qy 61 QLMKTERPRNTEIIRCLQWTTVIERTFHVETPEREETWTAIQTVDGLKKQ--EEEM 118
Db 61 QLMKTERPRNTEIIRCLQWTTVIERTFHVDSPEDEBEWTRAIQMVANSLKQRPQGEDAM 120

Qy 119 DFRSGPSDNGSABEMEVSIAKPKHRYTMNEFEYIKLLGKGTFGKVLVKEKATGRYYAM 178
Db 121 DYKCGSPSDSTSEMEVAVSKARAKVTMDNDFYLLKLGKGTFGKVLVREKATGRYYAM 180

Qy 179 KILKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSPQTHDLRCFVMEYANGGELFFH 238
Db 181 KILKEVIVAKDEVAHTVTSRVLQNRHPFLTALKYAFQTHDLRCFVMEYANGGDLFFH 240

Qy 239 LSRERFSEDRARFYGAIEIVSALDYHSEKNVVYRDLKLENLMDKDGHIKITDFGLCKE 298
Db 241 LSRERFTEDRARFYGAIEIVSALDYHLS--TDVVYRDLKLENLMDKDGHIKITDFGLSKE 299

Qy 299 GIKDGATMKTFCGTPPEYLAPEVLDDNDYGRAVDWGLGVVYEMWMCGRLPFYNQDHEKLF 358
Db 300 GISDGATMKTFCGTPPEYLAPEVLDDNDYGRAVDWGLGVVYEMWMCGRLPFYNQDHERLP 359

Qy 359 ELILMEIRPRTLGPKAKSLGGLKKDPKQRLGGSGSDAKETIMQHRFPAGIVQHVYE 418
Db 360 ELILMEIRPRTLGPKAKSLGGLKKDPKQRLGGSGSDAKETIMQHRFPAGIVQHVQ 419

Qy 419 KLSPPKPKQVTSFTDTRYFDEEFTAQWITTPDQDDSMCEVDSERRPHFPQFSYSAS 477
Db 420 KLLPFPKPKQVTSFTDTRYFDDDEFTAQWITTPDQDDSMCEVDSERRPHFPQFSYSAS 478

RESULT 14
ID _AKT3 HUMAN STANDARD; PRT; 479 AA.
AC Q9Y243; G96QV3; Q9UFP5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE RAC-gamma serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-gamma)
DE (Protein kinase Akt-3) (Protein kinase B, gamma) (PKB gamma) (STK-2).
GN Name=AKT3;
OS Homo sapiens (Human).
```

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OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS.
RX MEDLINE=99194749; PubMed=10092583; DOI=10.1074/jbc.274.14.9133;
RA Brodbeck D., Cron P., Hemmings B.A.;
RT "A human protein kinase B gamma with regulatory phosphorylation sites
in the activation loop and in the C-terminal hydrophobic domain.";
RL J. Biol. Chem. 274:9133-9136(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99225329; PubMed=10208883; DOI=10.1006/bbrc.1999.0559;
RA Nakatani K., Sakaue H., Thompson D.A., Weigel R.J., Roth R.A.;
RT "Identification of a human Akt3 (protein kinase B gamma) which
contains the regulatory serine phosphorylation site.";
RL Biochem. Biophys. Res. Commun. 257:906-910(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
MEDLINE=99421751; PubMed=10491192;
RA Masure S., Haefner B., Wesselink J.-J., Hoefnagel E., Mortier E.,
Verhasselt P., Tuytelaars A., Gordon R., Richardson A.;
RT "Molecular cloning, expression and characterization of the human
serine/threonine kinase Akt-3.";
RL Eur. J. Biochem. 265:353-360(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Li X., Yu L., Huang H., Zhang M., Zhao Y., Zhao S.;
RT "Cloning of a novel human cDNA, STK-2, which encodes a rat serine-
threonine protein kinase (STK) homolog.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Testis;
RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
Ansoerge W., Boecker M., Bloecker H., Bauersachs S., Blum H.,
Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
Mewes H.-W., Othenwaelder B., Obermaier B., Tampe J., Heubner D.,
Wambutt R., Korn B., Klein M., Foustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435(2001).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND MUTAGENESIS OF THR-305 AND
THR-447.
RX PubMed=11387345; DOI=10.1074/jbc.M104633200;
RA Brodbeck D., Hill M.M., Hemmings B.A.;
RT "Two splice variants of PKB gamma have different regulatory capacity
depending on the presence or absence of the regulatory phosphorylation
site Ser-472 in the C-terminal hydrophobic domain.";
RL J. Biol. Chem. 276:29550-29558(2001).
CC -1- FUNCTION: IGF-1 leads to the activation of AKT3, which may play a
role in regulating cell survival. Capable of phosphorylating
several known proteins. Truncated isoform 2/pKB gamma 1 without
the second serine phosphorylation site could still be stimulated
but to a lesser extent.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after
cell stimulation leading to its translocation.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=PKB gamma;
CC IsoId=Q9Y243-1; Sequence=Displayed;
CC Name=2; Synonyms=PKB gamma 1;
CC IsoId=Q9Y243-2; Sequence=VSP_004947;
CC -1- TISSUE SPECIFICITY: In adult tissues, it is highly expressed in
brain, lung and kidney, but weakly in heart, testis and liver. In
fetal tissues, it is highly expressed in heart, liver and brain
and not at all in kidney.
CC -1- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
kinase alpha (PI(3)K) results in its targeting to the plasma
```

CC membrane.  
 CC -1- PTM: Phosphorylated on threonine and serine residues.  
 CC Phosphorylation on both serines and threonines is required for  
 CC full activity.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC  
 CC subfamily.  
 CC -1- SIMILARITY: Contains 1 PH domain.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF124141; AAD29089.1; -  
 CC EMBL; AF135794; AAD24196.1; -  
 CC EMBL; AF085234; AAL40392.1; -  
 CC EMBL; AF245709; CAB53537.1; -  
 CC EMBL; AL117525; CAB55977.1; ALT\_TERM.  
 CC EMBL; AY005799; AAF91073.1; -  
 CC PIR; A59380; A59380.  
 CC HSSP; P31751; IGZK.  
 CC Inactive; Q9Y243; -  
 CC Genew; HGNC:393; AKT3.  
 CC GO; GO:0004672; F:protein kinase activity; TAS.  
 CC GO; GO:0006468; P:protein amino acid phosphorylation; TAS.  
 CC GO; GO:0007165; P:signal transduction; TAS.  
 CC InterPro; IPR011009; Kinase\_like.  
 CC InterPro; IPR001849; PH.  
 CC InterPro; IPR001036; PH related.  
 CC InterPro; IPR000961; Kinase\_C.  
 CC InterPro; IPR000719; Prot\_kinase.  
 CC InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 CC InterPro; IPR002290; Ser\_thr\_kinase.  
 CC Pfam; PF00169; PH; 1.  
 CC Pfam; PF00069; Pkinase; 1.  
 CC Pfam; PF00433; Pkinase\_C; 1.  
 CC ProDom; PD000001; Prot\_kinase; 1.  
 CC SMART; SM00233; PH; 1.  
 CC SMART; SM00220; S\_TK; 1.  
 CC SMART; SM00133; S\_TK\_X; 1.  
 CC PROSITE; PS50003; PH DOMAIN; 1.  
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 CC PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 CC PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 CC Alternative splicing; ATP-binding; Phosphorylation;  
 CC Serine/threonine-protein kinase; Transferase.  
 CC DOMAIN 5 107  
 CC PH.  
 CC DOMAIN 148 405  
 CC NP\_BIND 154 162  
 CC BINDING 177 177  
 CC ATP (By similarity).  
 CC Proton acceptor (By similarity).  
 CC Phosphoserine (By similarity).  
 CC Phosphothreonine (By similarity).  
 CC YDEGDQMDNRRRPHFPQFYSASGRE -> CQQSDCGML  
 CC GNWKK (in isoform 2).  
 CC /FTID-VSP 004947.  
 CC T->A: No activation after pervanadate  
 CC treatment.  
 CC T->D: 2-fold increase of phosphorylation  
 CC steady state level, no activation after  
 CC pervanadate treatment.  
 CC T->A: No effect.  
 CC T->D: No effect.  
 CC S->A: 67% decrease of activity after  
 CC pervanadate treatment.  
 CC S->D: 1.4-fold increase of  
 CC phosphorylation steady state level, 50%  
 CC decrease of activity after pervanadate  
 CC treatment.  
 CC MUTAGEN 305 305  
 CC T->A: 55774 MW; F08BDD6502E78FB CRC64;  
 CC MUTAGEN 305 305  
 CC T->D: 2-fold increase of phosphorylation  
 CC steady state level, no activation after  
 CC pervanadate treatment.  
 CC T->A: No effect.  
 CC T->D: No effect.  
 CC S->A: 67% decrease of activity after  
 CC pervanadate treatment.  
 CC S->D: 1.4-fold increase of  
 CC phosphorylation steady state level, 50%  
 CC decrease of activity after pervanadate  
 CC treatment.  
 CC MUTAGEN 447 447  
 CC T->A: 55774 MW; F08BDD6502E78FB CRC64;  
 CC MUTAGEN 447 447  
 CC T->D: 2-fold increase of phosphorylation  
 CC steady state level, no activation after  
 CC pervanadate treatment.  
 CC T->A: No effect.  
 CC T->D: No effect.  
 CC S->A: 67% decrease of activity after  
 CC pervanadate treatment.  
 CC S->D: 1.4-fold increase of  
 CC phosphorylation steady state level, 50%  
 CC decrease of activity after pervanadate  
 CC treatment.  
 CC MUTAGEN 472 472  
 CC T->A: 55774 MW; F08BDD6502E78FB CRC64;  
 CC MUTAGEN 472 472  
 CC T->D: 2-fold increase of phosphorylation  
 CC steady state level, no activation after  
 CC pervanadate treatment.  
 CC T->A: No effect.  
 CC T->D: No effect.  
 CC S->A: 67% decrease of activity after  
 CC pervanadate treatment.  
 CC S->D: 1.4-fold increase of  
 CC phosphorylation steady state level, 50%  
 CC decrease of activity after pervanadate  
 CC treatment.  
 CC MUTAGEN 479 AA; 55774 MW; F08BDD6502E78FB CRC64;  
 CC SEQUENCE 479 AA; 55774 MW; F08BDD6502E78FB CRC64;  
 CC

Query Match 82.6%; Score 2105.5; DB 1; Length 479;  
 Best Local Similarity 82.7%; Pred. No. 1.4e-124;  
 Matches 397; Conservative 36; Mismatches 42; Indels 5; Gaps 4;  
 QY 1 MSDVAIVKEGWLHKGREYIKTRPRYFLKNDGTFYIGYKRPQDVDOREAPLNPFVAQC 60  
 DB 1 MSDVTIVKEGVQKRGYIKNRPYFLKTDGTFYIGYKRPQDVDP-LPYPLNPFVAKC 59  
 QY 61 QLMKTERPRNTFIIRCLQMTVTIERTFHVETPEREETTAIQTVDAGLKKQEEEMDF 120  
 DB 60 QLMKTERPKNTFIIRCLQMTVTIERTFHVDTPEREETWTAIQAVADRLQREERMC 119  
 QY 121 RSGSPSNSGAEMEVSALRKPRTVWNEPYLKLCKGTFGKVLKKEKATGRYAMKI 180  
 DB 120 SPTSQIDNIGEEEMDASTTHHK-RKTWNDFYLLKLGTFGKVLVREKASGKYAMKI 178  
 QY 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSPQTHDRLCFVMEYANGGELFFHLS 240  
 DB 179 LKKEVIAKDEVAHTLTESRVLKNTRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLS 238  
 QY 241 RERVSEDRARFYGAETVSALDYLSHKNVYRDLKLENMLDKDGHKIKITDFGLCKEGI 300  
 DB 239 RERVSEDRTRFYGAETVSALDYLSHSGK-IVYRDLKLENMLDKDGHKIKITDFGLCKEGI 297  
 QY 301 KDGMTKTCGTPYLAPEVLENDYDGRAVDWGLGVVMEYEMCGRLPFYNODHEKLPFEL 360  
 DB 298 TDAATMTKTCGTPYLAPEVLENDYDGRAVDWGLGVVMEYEMCGRLPFYNODHEKLPFEL 357  
 QY 361 ILMEIIRFPRTLGPKEAKSLGLLKDPKORLGGSDAKEIMQHRFPAGIVWQHVYBKK 420  
 DB 358 ILMEDIKFPRTLSSDAKSLGLLKDPKNKLGSGPDPAKEIMRHSFSGVYVQDVYDKK 417  
 QY 421 LSPFPKPQVTSSETDTRVDEEFTAQMITITPPDQ-DDSMECVDSERRPFPQFSYSASG 478  
 DB 418 LVPFPKPQVTSSETDTRVDEEFTAQMITITPPDQ-DGMDNRRRPHFPQFSYSASG 477  
 RESULT 15  
 Q61P76 PRELIMINARY; PRT; 485 AA.  
 ID Q61P76  
 AC Q61P76;  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE MGC78893 protein.  
 GN Name=MGC78893;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen.  
 RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Berger J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 23, 2005, 20:38:14 : Search time 42 Seconds  
(without alignments)  
1099.620 Million cell updates/sec

Title: US-10-621-485A-1  
Perfect score: 2550  
Sequence: 1 MSDVAIVKEGWLKRGVEIK.....VDSERRPHFPQFSASGTA 480  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID       | Description        |
|------------|--------|-------------|--------|----------|--------------------|
| 1          | 2544   | 99.8        | 480    | 1 A39360 | protein kinase (EC |
| 2          | 2509   | 98.4        | 480    | 1 S33364 | protein kinase (EC |
| 3          | 2509   | 98.4        | 763    | 1 A40831 | gag-akt polyprotei |
| 4          | 2507   | 98.3        | 480    | 1 J24337 | protein kinase (EC |
| 5          | 2452   | 96.2        | 480    | 1 S62117 | protein kinase (EC |
| 6          | 2126.5 | 83.4        | 481    | 1 A46288 | protein kinase (EC |
| 7          | 2113.5 | 82.9        | 481    | 1 J24338 | protein kinase (EC |
| 8          | 2105.5 | 82.6        | 479    | 1 A59380 | protein kinase (EC |
| 9          | 2008.5 | 78.8        | 462    | 1 T17287 | protein kinase (EC |
| 10         | 1989.5 | 78.0        | 454    | 1 J43435 | protein kinase (EC |
| 11         | 1581.5 | 62.0        | 611    | 1 A55888 | protein kinase (EC |
| 12         | 1490.5 | 58.5        | 546    | 1 T43233 | protein kinase (EC |
| 13         | 1470   | 57.6        | 541    | 1 T43232 | protein kinase (EC |
| 14         | 1390.5 | 54.5        | 528    | 1 T21523 | protein kinase (EC |
| 15         | 1324   | 51.9        | 483    | 1 T43234 | protein kinase (EC |
| 16         | 855    | 33.5        | 671    | 1 K1HUC1 | protein kinase C ( |
| 17         | 854    | 33.5        | 736    | 1 K1RBC2 | protein kinase C ( |
| 18         | 853    | 33.5        | 671    | 1 K1RBC1 | protein kinase C ( |
| 19         | 853    | 33.5        | 1102   | 2 T28666 | protein kinase C-r |
| 20         | 852    | 33.4        | 431    | 2 A48094 | serum and glucocor |
| 21         | 852    | 33.4        | 671    | 1 K1R1C1 | protein kinase C ( |
| 22         | 849.5  | 33.3        | 683    | 1 A23690 | protein kinase (EC |
| 23         | 848.5  | 33.3        | 737    | 1 K1M5C2 | protein kinase C ( |
| 24         | 847.5  | 33.2        | 737    | 1 K1M5C1 | protein kinase C ( |
| 25         | 845.5  | 33.2        | 682    | 1 S29478 | protein kinase C ( |
| 26         | 842    | 33.0        | 682    | 1 A39666 | protein kinase C ( |
| 27         | 840.5  | 33.0        | 737    | 1 K1R1C2 | protein kinase C ( |
| 28         | 837    | 32.8        | 1096   | 1 S61917 | protein kinase C ( |
| 29         | 833    | 32.7        | 1016   | 1 A46079 | protein kinase C ( |

|    |       |      |      |          |                    |
|----|-------|------|------|----------|--------------------|
| 30 | 831.5 | 32.6 | 984  | 2 S67537 | protein kinase (EC |
| 31 | 828   | 32.5 | 547  | 2 T22856 | hypothetical prote |
| 32 | 828   | 32.5 | 988  | 1 S35362 | protein kinase C ( |
| 33 | 826.5 | 32.4 | 586  | 2 A53758 | protein kinase C ( |
| 34 | 826.5 | 32.4 | 587  | 2 A49509 | protein kinase C ( |
| 35 | 826.5 | 32.4 | 634  | 1 B32392 | protein kinase C ( |
| 36 | 826.5 | 32.4 | 673  | 1 K1HUC2 | protein kinase C ( |
| 37 | 826.5 | 32.4 | 673  | 2 S11213 | protein kinase C ( |
| 38 | 825   | 32.4 | 707  | 1 A53530 | protein kinase C ( |
| 39 | 825   | 32.4 | 1174 | 2 T43051 | protein kinase C ( |
| 40 | 824.5 | 32.3 | 673  | 1 K1RBC2 | protein kinase C ( |
| 41 | 823.5 | 32.3 | 673  | 1 K1R1C2 | protein kinase C ( |
| 42 | 823.5 | 32.3 | 673  | 1 K1BOC2 | protein kinase C ( |
| 43 | 820.5 | 32.2 | 672  | 1 K1BOC  | protein kinase C ( |
| 44 | 818.5 | 32.1 | 672  | 1 K1R1C  | protein kinase C ( |
| 45 | 817.5 | 32.1 | 672  | 1 K1HUC4 | protein kinase C ( |

## ALIGNMENTS

## RESULT 1

A39360  
protein kinase (EC 2.7.1.37) akt1 [validated] - human  
N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote  
C:Species: Homo sapiens (man)  
C>Date: 20-Mar-1992 #sequence\_revision 12-May-1994 #text\_change 16-Aug-2004  
C:Accession: A39360; S18000; S20836  
R:Jones, P.F.; Jakubowicz, T.; Pitossi, F.J.; Maurer, F.; Hemmings, B.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 4171-4175, 1991  
A:Title: Molecular cloning and identification of a serine/threonine protein kinase of th  
A:Reference number: A39360; MUID:912339529; PMID:1851997  
A:Accession: A39360  
A:Molecule type: mRNA  
A:Residues: 1-480 <JON>  
A:Cross-references: UNIPROT:P31749; GB:M63167; NID:g190827; PIDN:AAA36539.1; PID:g190828  
R:Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 205, 1217, 1992  
A:Reference number: S24423; MUID:92249329; PMID:1533586  
A:Contents: erratum  
A:Accession: S36389  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 63-172, 'A', 175-201, 'Q', 203-211, 'R', 213-245, 'A', 247-408, 'T', 410-475, 'P', 477, '  
A:Cross-references: EMBL:X61037; NID:g35480; PIDN:CAA43372.1; PID:g35481  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1991  
R:Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 201, 475-481, 1991  
A:Title: Molecular cloning and characterisation of a novel putative protein-serine kinas  
A:Reference number: S17999; MUID:92037600; PMID:1718748  
A:Accession: S18000  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 63-70, 'TPSSAACSGPLSSNAPSMWRLRSGVDNRHPCGRRPQ', 'EAGGGDGLPVGLTQRLRGRDGGV'  
A:Cross-references: EMBL:X61037  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991  
R:Coffer, P.  
submitted to the EMBL Data Library, July 1991  
A:Reference number: S20836  
A:Accession: S20836  
A:Molecule type: mRNA  
A:Residues: 63-70, 'TPSSAACSGPLSSNAPSMWRLRSGVDNRHPCGRRPQ', 'EAGGGDGLPVGLTQRLRGRDGGV'  
A:Cross-references: EMBL:X61037  
A:Note: this sequence has been revised in reference S24423  
R:Alessi, D.R.; Andjelkovic, M.; Caudwell, B.; Cron, P.; Morrice, N.; Cohen, P.; Hemming  
EMBO J. 15, 6541-6551, 1996  
A:Title: Mechanism of activation of protein kinase B by insulin and IGF-1.  
A:Reference number: A6192; MUID:97133284; PMID:8978681  
A:Contents: annotation; phosphorylation sites  
R:Toker, A.; Newton, A.C.  
J. Biol. Chem. 275, 8271-8274, 2000

A;Title: Akt/protein kinase B is regulated by autophosphorylation at the hypothetical pS3364  
A;Reference number: A64193; MUID:20187529; PMID:10722653  
A;Contents: annotation; autophosphorylation site  
C;Comment: Akt1 is ubiquitous as an inactive multimeric complex. It binds phosphatidyl-3-nt protein kinase 1 complex. Akt1 can then autophosphorylate and become fully active.  
C;Genetics:  
A;Gene: GDB:AKT1; RAC; PKB  
A;Cross-references: GDB:118989; OMIM:164730  
A;Map position: 14q32.32-14q32.32  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine  
A;Pathway: signal transduction pathways regulating various processes including insulin a  
e production  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene  
F:4-106/Domain: pleckstrin repeat homology <PLK>  
F:148-408/Domain: protein kinase homology <KIN>  
F:156-164/Region: protein kinase ATP-binding motif  
F:179/Active site: Lys #status predicted  
F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki  
F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status experime

Query Match 99.8%; Score 2544; DB 1; Length 480;  
Best Local Similarity 99.8%; Pred. No. 1.9e-101;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGHLKRGGEYIKTWPRYFLKNDGTFIGYKRPQDVDDREAPLNFSVAQC 60  
Db 1 MSDVAIVKEGHLKRGGEYIKTWPRYFLKNDGTFIGYKRPQDVDDREAPLNFSVAQC 60

Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKOEEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKOEEEMDF 120

Qy 121 RSGSPDSNGABEEMVSLAKPKHVTWNEFEYILKLGKTFGKVILVKEKATGRYYAMKI 180  
Db 121 RSGSPDSNGABEEMVSLAKPKHVTWNEFEYILKLGKTFGKVILVKEKATGRYYAMKI 180

Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELPFHLS 240  
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELPFHLS 240

Qy 241 RERVFSDDRARFYGAETVSALDYHSEKNVYVYRDLENLMLDKDGHIKITDFGLCKEGI 300  
Db 241 RERVFSDDRARFYGAETVSALDYHSEKNVYVYRDLENLMLDKDGHIKITDFGLCKEGI 300

Qy 301 KOGATMTKTCGTPPEYLAPEVLENDYGRAVDWNGLVGVVYEMMCGRLPFYVQDHEKLFEL 360  
Db 301 KOGATMTKTCGTPPEYLAPEVLENDYGRAVDWNGLVGVVYEMMCGRLPFYVQDHEKLFEL 360

Qy 361 ILMEERFPRTLGPPEAKSLLSGLLKDPKQRLGGSDAKKEIMQHRFFAGIVQHVYVEKK 420  
Db 361 ILMEERFPRTLGPPEAKSLLSGLLKDPKQRLGGSDAKKEIMQHRFFAGIVQHVYVEKK 420

Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPQDDSMCEVDSERRRPHFPQFSYASGTA 480  
Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPQDDSMCEVDSERRRPHFPQFSYASGTA 480

RESULT 2  
S33364  
protein kinase (EC 2.7.1.37) akt1 [similarity] - mouse  
N;Alternate names: protein kinase B alpha; RAC-PK-alpha;  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Aug-2004  
C;Accession: S33364  
R;Bellacosa, A.; Franke, T.F.; Gonzalez-Portal, M.E.; Datta, K.; Taguchi, T.; Gardner, J  
Oncogene 8, 745-754, 1993  
A;Title: Structure, expression and chromosomal mapping of c-akt: relationship to v-akt a  
A;Reference number: S33364; MUID:93173519; PMID:8437858  
A;Accession: S33364  
A;Status: preliminary  
A;Molecule type: mRNA

A;Residues: 1-480 <BEL>  
A;Cross-references: UNIPROT:P31750; EMBL:X65687; NID:g287806; PIDN:CAA46620.1; PID:g2878  
C;Genetics:  
A;Gene: MGI:Akt  
A;Cross-references: MGI:87986  
A;Map position: 12  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
A;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene  
F:4-106/Domain: pleckstrin repeat homology <PLK>  
F:148-408/Domain: protein kinase homology <KIN>  
F:156-164/Region: protein kinase ATP-binding motif  
F:179/Active site: Lys #status predicted  
F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki  
F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicte

Query Match 98.4%; Score 2509; DB 1; Length 480;  
Best Local Similarity 98.3%; Pred. No. 5.9e-100;  
Matches 472; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGHLKRGGEYIKTWPRYFLKNDGTFIGYKRPQDVDDREAPLNFSVAQC 60  
Db 1 MNDVAIVKEGHLKRGGEYIKTWPRYFLKNDGTFIGYKRPQDVDDQRESPLNFSVAQC 60

Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKOEEEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKOEEETWDF 120

Qy 121 RSGSPDSNGABEEMVSLAKPKHVTWNEFEYILKLGKTFGKVILVKEKATGRYYAMKI 180  
Db 121 RSGSPDSNGABEEMVSLAKPKHVTWNEFEYILKLGKTFGKVILVKEKATGRYYAMKI 180

Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELPFHLS 240  
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELPFHLS 240

Qy 241 RERVFSDDRARFYGAETVSALDYHSEKNVYVYRDLENLMLDKDGHIKITDFGLCKEGI 300  
Db 241 RERVFSDDRARFYGAETVSALDYHSEKNVYVYRDLENLMLDKDGHIKITDFGLCKEGI 300

Qy 301 KOGATMTKTCGTPPEYLAPEVLENDYGRAVDWNGLVGVVYEMMCGRLPFYVQDHEKLFEL 360  
Db 301 KOGATMTKTCGTPPEYLAPEVLENDYGRAVDWNGLVGVVYEMMCGRLPFYVQDHEKLFEL 360

Qy 361 ILMEERFPRTLGPPEAKSLLSGLLKDPKQRLGGSDAKKEIMQHRFFAGIVQHVYVEKK 420  
Db 361 ILMEERFPRTLGPPEAKSLLSGLLKDPKQRLGGSDAKKEIMQHRFFAGIVQHVYVEKK 420

Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPQDDSMCEVDSERRRPHFPQFSYASGTA 480  
Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPQDDSMCEVDSERRRPHFPQFSYASGTA 480

RESULT 3  
A40831  
gag-akt polyprotein - AKT8 murine leukemia virus  
N;Contains: amino end of core protein p30; core protein p15; inner coat protein p12; kin  
C;Species: AKT8 murine leukemia virus  
C;Date: 12-Feb-1993 #sequence\_revision 12-May-1994 #text\_change 16-Aug-2004  
C;Accession: A40831; B40831  
R;Bellacosa, A.; Testa, J.R.; Staal, S.P.; Tsichlis, P.N.  
Science 254, 274-277, 1991  
A;Title: A retroviral oncogene, akt, encoding a serine-threonine kinase containing an SH  
A;Reference number: A40831; MUID:92022574; PMID:1833819  
A;Accession: A40831  
A;Molecule type: DNA  
A;Residues: 1-262 <BEL>  
A;Cross-references: GB:M80675  
A;Accession: B40831  
A;Molecule type: DNA  
A;Residues: 262-763 <BE2>



A;Cross-references: GB:M80675  
C;Genetics:  
A;Gene: gag-akt  
C;Superfamily: pleckstrin repeat homology; protein kinase homology  
C;Keywords: ATP; core protein; glycoprotein; oncogene; phosphoprotein; phosphotransferase  
F;1-129/Product: core protein p15 #status predicted <CP1>  
F;130-214/Product: inner coat protein p12 #status predicted <CP2>  
F;284-763/Product: kinase-related transforming protein akt #status predicted <AKT>  
F;287-389/Domain: pleckstrin repeat homology <PLK>  
F;431-691/Domain: protein kinase homology <KIN>  
F;439-447/Region: protein kinase ATP-binding motif  
F;25-337/Binding site: carbohydrate (Aen) (covalent) #status predicted  
F;462/Active site: Lys #status predicted  
F;609/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 98.4%; Score 2509; DB 1; Length 763;  
Best Local Similarity 98.3%; Pred. No. 8.8e-100;  
Matches 472; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDQVDQREAPLNFSVAQC 60  
Db 284 MNDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDQVDQREAPLNFSVAQC 343  
Qy 61 QLMKTERPRNTFIIRCLQMTTIVERTFHVETPEREETWTAIQTVDGLKQREEMDF 120  
Db 344 QLMKTERPRNTFIIRCLQMTTIVERTFHVETPEREETWTAIQTVDGLKQREEMDF 403  
Qy 121 RSGSPSDNSGAEMEVSIAKPKHRTVMNEFYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
Db 404 RSGSPSDNSGAEMEVSIAKPKHRTVMNEFYLLKLGKGTGKVLVKEKATGRYYAMKI 463  
Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALYKSFQTHDRLCFVMEYANGGELFFHLS 240  
Db 464 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALYKSFQTHDRLCFVMEYANGGELFFHLS 523  
Qy 241 RERVSEDRARFYGAIEVSALDYLSHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Db 524 RERVSEDRARFYGAIEVSALDYLSHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 583  
Qy 301 KDGATMTKTCGTPPYLAPEVLENDYGRAVDWGLGVVMEYANGGELFFHLS 360  
Db 584 KDGATMTKTCGTPPYLAPEVLENDYGRAVDWGLGVVMEYANGGELFFHLS 643  
Qy 361 LMEEIIRPRTLGPPEAKSLGLLKDPKQRLGGGSEDAKEMOHRFPAGIVWQDVYEKK 420  
Db 644 LMEEIIRPRTLGPPEAKSLGLLKDPKQRLGGGSEDAKEMOHRFPAGIVWQDVYEKK 703  
Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYASGTA 480  
Db 704 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYASGTA 763

RESULT 4  
JC2437  
Protein kinase (EC 2.7.1.37) akt1 [validated] - rat  
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
A;Accession: JC2437  
R;Konishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.  
Biochem. Biophys. Res. Commun. 205, 817-825, 1994  
A;Title: Molecular cloning of rat RAC protein kinase alpha and beta and their associati  
A;Reference number: JC2437; MUID:95091823; PMID:7999118  
A;Accession: JC2437  
A;Molecule type: mRNA  
A;Residues: 1-480 <KON>  
A;Cross-references: UNIPROT:P47196; DBJ:D30040; NID:G485402; PIDN:BAA06279.1; PID:G4854  
A;Experimental source: testis  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene

F;4-106/Domain: pleckstrin repeat homology <PLK>  
F;148-408/Domain: protein kinase homology <KIN>  
F;156-164/Region: protein kinase ATP-binding motif  
F;179/Active site: Lys #status predicted  
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki  
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicte

Query Match 98.3%; Score 2507; DB 1; Length 480;  
Best Local Similarity 98.1%; Pred. No. 7.1e-100;  
Matches 471; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDQVDQREAPLNFSVAQC 60  
Db 1 MNDVAIVKEGWLHKGGEYIKTRPRYFLKNDGTFIGYKERPDQVDQREAPLNFSVAQC 60  
Qy 61 QLMKTERPRNTFIIRCLQMTTIVERTFHVETPEREETWTAIQTVDGLKQREEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQMTTIVERTFHVETPEREETWTAIQTVDGLKQREEMDF 120  
Qy 121 RSGSPSDNSGAEMEVSIAKPKHRTVMNEFYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
Db 121 RSGSPSDNSGAEMEVSIAKPKHRTVMNEFYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALYKSFQTHDRLCFVMEYANGGELFFHLS 240  
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALYKSFQTHDRLCFVMEYANGGELFFHLS 240  
Qy 241 RERVSEDRARFYGAIEVSALDYLSHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Db 241 RERVSEDRARFYGAIEVSALDYLSHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300  
Qy 301 KDGATMTKTCGTPPYLAPEVLENDYGRAVDWGLGVVMEYANGGELFFHLS 360  
Db 301 KDGATMTKTCGTPPYLAPEVLENDYGRAVDWGLGVVMEYANGGELFFHLS 360  
Qy 361 LMEEIIRPRTLGPPEAKSLGLLKDPKQRLGGGSEDAKEMOHRFPAGIVWQDVYEKK 420  
Db 361 LMEEIIRPRTLGPPEAKSLGLLKDPKQRLGGGSEDAKEMOHRFPAGIVWQDVYEKK 420  
Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYASGTA 480  
Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSYASGTA 480

RESULT 5  
S62117  
protein kinase (EC 2.7.1.37) akt1 [similarity] - bovine  
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Aug-2004  
A;Accession: S62117; S24423; S17999; S15714; S36388  
R;Coffer, P.J.; Woodgett, J.R.  
submitted to the EMBL Data Library, December 1991  
A;Reference number: S62117  
A;Accession: S62117  
A;Molecule type: mRNA  
A;Residues: 1-480 <COF>  
A;Cross-references: UNIPROT:Q01314; EMBL:X61036; NID:G630; PIDN:CAA43371.1; PID:G631  
A;Note: this is a revision to the sequence from reference S17999  
R;Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 205, 1217, 1992  
A;Reference number: S24423; MUID:92249329; PMID:1533586  
A;Contents: erratum  
A;Accession: S24423  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 70-78, N', 80-145 <COW>  
A;Cross-references: EMBL:X61036  
A;Note: this is a revision to the sequence from reference S17999  
R;Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 201, 475-481, 1991  
A;Title: Molecular cloning and characterisation of a novel putative protein-serine kinas  
A;Reference number: S17999; MUID:92037600; PMID:1718748

A;Accession: S17999  
A;Molecule type: mRNA  
A;Residues: 1-70,"TPSSAACGPRSSARSTWRRPRSGVDHRRPDGRRQAAGGGDGLPVGLTRRELGRGDGVAGQA  
A;Cross-references: EMBL:X61036  
A;Note: this sequence has been revised in references S62117 and S24423  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene  
F;4-106/Domain: pleckstrin repeat homology <PLK>  
F;148-408/Domain: protein kinase homology <KIN>  
F;156-164/Region: protein kinase ATP-binding motif  
F;179/Active site: Lys #status predicted  
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki  
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicte

Query Match 96.2%; Score 2452; DB 1; Length 480;  
Best Local Similarity 96.2%; Pred. No. 1.5e-97;  
Matches 462; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKERPDQVDQREAPLNFSVAQC 60  
Db 1 MNDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKERPDQREAPLNFSVAQC 60

Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKQREEMDF 120  
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKQREEMDF 120

Qy 121 RSGSPDSNGAEEMVSLAKPKHRTVMNEFYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
Db 121 RSGSPDSNGAEEMVSLAKPKHRTVMNEFYLLKLGKTFGKVLVKEKATGRYYAMKI 180

Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLS 240  
Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLS 240

Qy 241 RERVSEDRARFYGAETVSALDYLHSEKNVYVRDLKLENMLDKDGHKIKITDFGLCKEGI 300  
Db 241 RERVSEDRARFYGAETVSALDYLHSEKNVYVRDLKLENMLDKDGHKIKITDFGLCKEGI 300

Qy 301 KDGATMTKTCGTPPYLAPEVLEDNDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
Db 301 KDGATMTKTCGTPPYLAPEVLEDNDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360

Qy 361 ILMEEIFRPRTLSPKSLGLLKDQPKORLGGSDAKEIMQHRFFAGIVMOWHYEKK 420  
Db 361 ILMEEIFRPRTLSPKSLGLLKDQPKORLGGSDAKEIMQHRFFAGIVMOWHYEKK 420

Qy 421 LSPPFKPQVTSSETDTRYFDEEFTAQMITITPPDQDSDMECVDSERRRPHFPQFSYSASGTA 480  
Db 421 LSPPFKPQVTSSETDTRYFDEEFTAQMITITPPDQDSDMECVDSERRRPHFPQFSYSASATA 480

RESULT 6  
A46288  
protein kinase (EC 2.7.1.37) akt2 - human  
N;Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein  
C;Species: Homo sapiens (man)  
C;Date: 22-Sep-1993 #sequence\_revision 12-May-1994 #text\_change 16-Aug-2004  
C;Accession: A46288  
R;Cheng, J.Q.; Godwin, A.K.; Bellacosa, A.; Taguchi, T.; Franke, T.F.; Hamilton, T.C.; T  
Proc. Natl. Acad. Sci. U.S.A. 89, 9267-9271, 1992  
A;Title: AKT2, a putative oncogene encoding a member of a subfamily of protein-serine/th  
A;Reference number: A46288; MUID:93028445; PMID:11409633  
A;Accession: A46288  
A;Molecule type: mRNA  
A;Residues: 1-481 <CHE>  
A;Cross-references: UNIPROT:P31751; GB:M95936; NID:g178325; PIDN:AAA58364.1; PID:g178326  
A;Note: sequence extracted from NCI backbone (NCBIP:115859)  
C;Comment: This protein is amplified in some pancreatic, ovarian, and other carcinomas.  
C;Genetics:  
A;Gene: GDB:AKT2

A;Cross-references: GDB:135660; OMIM:164731  
A;Map position: 19q13.2-19q13.2  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k  
F;4-106/Domain: pleckstrin repeat homology <PLK>  
F;150-409/Domain: protein kinase repeat homology <KIN>  
F;158-166/Region: protein kinase ATP-binding motif  
F;181/Active site: Lys #status predicted

Query Match 83.4%; Score 2126.5; DB 1; Length 481;  
Best Local Similarity 81.6%; Pred. No. 9.6e-84;  
Matches 391; Conservative 52; Mismatches 33; Indels 3; Gaps 2;

Qy 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFIGYKERPDQVDQREAPLNFSVAQC 60  
Db 1 MNEVSVIKEGWLHKGRIYKTRPRYFLKSDSGFIGYKERPEAPDQTLPLNNFSVAEC 60

Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAIQTVADGLKKOE--EEM 118  
Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVDSDEDEEMWRAIQWVANSLKQAPGSDPM 120

Qy 119 DFRSGSPDSNGAEEMVSLAKPKHRTVMNEFYLLKLGKTFGKVLVKEKATGRYYAM 178  
Db 121 DYKCGSPDSSTTEEMEVASVAKAVTMNDFYLLKLGKTFGKVLVKEKATGRYYAM 180

Qy 179 KILKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFPH 238  
Db 181 KILRKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYAFQTHDRLCFVMEYANGGELFPH 240

Qy 239 LSRERVSEDRARFYGAETVSALDYLHSEKNVYVRDLKLENMLDKDGHKIKITDFGLCKE 298  
Db 241 LSRERVSEDRARFYGAETVSALDYLHSEKNVYVRDLKLENMLDKDGHKIKITDFGLCKE 299

Qy 299 GIKDGATMTKTCGTPPYLAPEVLEDNDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLF 358  
Db 300 GISDGATMTKTCGTPPYLAPEVLEDNDYGRAVDWGLGVVYEMMCGRLPFYVQDHERLF 359

Qy 359 ELILMEEIFRPRTLSPKSLGLLKDQPKORLGGSDAKEIMQHRFFAGIVMOWHYE 418  
Db 360 ELILMEEIFRPRTLSPKSLGLLKDQPKORLGGSDAKEIMVMEHRFFLSINWQDVVQ 419

Qy 419 KLSPPFKPQVTSSETDTRYFDEEFTAQMITITPPDQDSDMECVDSERRRPHFPQFSYSAS 477  
Db 420 KLLPFPKPQVTSSETDTRYFDEEFTAQSIITPPDRYDSLGLLELDQRTFFPQFSYSAS 478

RESULT 7  
JC2438  
protein kinase (EC 2.7.1.37) akt2 [validated] - rat  
N;Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: JC2438  
R;Konishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.  
Biochem. Biophys. Res. Commun. 205, 817-825, 1994  
A;Title: Molecular cloning of rat RAC protein kinase alpha and beta and their associatio  
A;Reference number: JC2437; MUID:95091823; PMID:7999118  
A;Accession: JC2438  
A;Molecule type: mRNA  
A;Residues: 1-481 <KON>  
A;Cross-references: UNIPROT:P47197; DDBJ:D30041; NID:g485404; PIDN:BAAO6280.1; PID:g485404  
A;Experimental source: testis  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes including myoblast  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k  
F;4-106/Domain: pleckstrin repeat homology <PLK>  
F;150-409/Domain: protein kinase repeat homology <KIN>  
F;158-166/Region: protein kinase ATP-binding motif

F:181/Active site: Lys #status predicted

Query Match 82.9%; Score 2113.5; DB 1; Length 481;  
 Best Local Similarity 81.4%; Pred. No. 3.4e-83;  
 Matches 390; Conservative 52; Mismatches 34; Indels 3; Gaps 2;  
 1 MSDVAIVKQGLHKKGEYIKTRPRYFLKNDGTFIGYKERPDQVDQREAPLNPFVSAQC 60  
 1 MNEVSIVKQGLHKKGEYIKTRPRYFLKSDGSFIGYKERPEADQTLPLNPFVSAEC 60  
 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREWTTAIQTVADGLKKQ--EBEEM 118  
 61 QLMKTERPRNTFVIRCLQWTTVIERTFHVDSPEEREWIRAIQMVANSLKQRGGEDAM 120  
 119 DFRSGSPDNGSAEMEVSILAKPKHVRVWNEFEYILKLGKTFGKVLVKEKATGRYYAM 178  
 121 DYKSGSPDSDSTSEMMEVAVSKARAKVTMNDFDYILKLGKTFGKVLVREKATGRYYAM 180  
 179 KILKEVIAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFH 238  
 181 KILKEVIAKDEVAHTTESRVLQNTRHPLTALKYAFQTHDRLCFVMEYANGGDLFFH 240  
 239 LSRERVSFEDRARFYGAIVSALDYHSEKNVYRDLEKLENMLDKDGHIKITDFGLCKE 298  
 241 LSRERVSFEDRARFYGAIVSALEYLHS-TDYYRDIKLENMLDKDGHIKITDFGLSKE 299  
 299 GIKGATMTKTCGTPPEYLAPEVLENDYGRAVDWGLGVVMYEMMCGRLPFYNQDHEKLP 358  
 300 GISDGAATMTKTCGTPPEYLAPEVLENDYGRAVDWGLGVVMYEMMCGRLPFYNQDHERLF 359  
 359 ELILMEERFPRTLGPEAKSLGLKKDKPKQRLGGGSDAKETIMOHRRFAGIYVQHVYE 418  
 360 ELILMEERFPRTLGPEAKSLGLKKDKPKQRLGGGSDAKEVMEHRRFFISINQDVVQ 419  
 419 KKLSPFPKQVTSFDTFYDEEFTAQMITITPPDQDSDMECVDSERRPFPQFSYSAS 477  
 420 KKLSPFPKQVTSFDTFYDEEFTAQMITITPPDQDSDMECVDSERRPFPQFSYSAS 478

RESULT 8  
 A:59380  
 N:Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
 C:Accession: A59380; A59379  
 J:Brodebeck, D.; Cron, P.; Hemmings, B.A.  
 A:Title: A human protein kinase Bgamma with regulatory phosphorylation sites in the acti  
 A:Reference number: A59380; MUID:99194749; PMID:10092583  
 A:Accession: A59380  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-479 <BRO>  
 R:Maure, S.; Haefner, B.; Wesselsink, J.J.; Hoefnagel, E.; Mortier, E.; Verhaseelt, P.;  
 Eur. J. Biochem. 265, 353-360, 1999  
 A:Title: Molecular cloning, expression and characterization of the human serine/threonin  
 A:Reference number: A59379; MUID:99421751; PMID:10491192  
 A:Accession: A59379  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-479 <MAS>  
 C:Cross-references: GB:CAB53537; NID:g5804886; PIDN:CAB53537.1  
 C:Genetics:  
 A:Gene: GDB:AKT3; PKBG; PRKBG; RAC-gamma  
 A:Cross-references: GDB:9954867  
 A:Map position: lq44-lq44  
 C:Function:  
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
 A:Pathway: signal transduction pathways regulating various processes  
 C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
 C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene

F:7-108/Domain: pleckstrin repeat homology <PLK>  
 F:149-408/Domain: protein kinase homology <KIN>  
 F:157-165/Region: protein kinase ATP-binding motif  
 F:177/Active site: Lys #status predicted  
 F:305/Binding site: phosphate (Thr) (covalent) #status predicted  
 F:474/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 82.6%; Score 2105.5; DB 1; Length 479;  
 Best Local Similarity 82.7%; Pred. No. 7.4e-83;  
 Matches 397; Conservative 36; Mismatches 42; Indels 5; Gaps 4;  
 1 MSDVAIVKQGLHKKGEYIKTRPRYFLKNDGTFIGYKERPDQVDQREAPLNPFVSAQC 60  
 1 MSDVTIVKQGLHKKGEYIKTRPRYFLKTDGSGFIGYKEKPDVD-LPYPLNPFVSAKC 59  
 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREWTTAIQTVADGLKKQBEEMDF 120  
 60 QLMKTERPKNTFIIRCLQWTTVIERTFHVDTPEEREWTBAIQAVDLRQREBERMNC 119  
 121 RSGSPDNGSAEMEVSILAKPKHVRVWNEFEYILKLGKTFGKVLVKEKATGRYYAMKI 180  
 120 SPTSOINIGEEEMDASTTHHK-RKTMNDFDYILKLGKTFGKVLVREKASGRYYAMKI 178  
 181 LKKEVIAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
 179 LKKEVIAKDEVAHTLTESRVLQNTRHPLTSLKYSFQTKDRLCFVMEYANGGELFFHLS 238  
 241 RERVFSFEDRARFYGAIVSALDYHSEKNVYRDLEKLENMLDKDGHIKITDFGLCKEGI 300  
 239 RERVFSFEDRARFYGAIVSALDYHSGK-IYVRDLKLENMLDKDGHIKITDFGLCKEGI 297  
 301 KDGATMTKTCGTPPEYLAPEVLENDYGRAVDWGLGVVMYEMMCGRLPFYNQDHEKLP 360  
 298 TDAATMTKTCGTPPEYLAPEVLENDYGRAVDWGLGVVMYEMMCGRLPFYNQDHEKLP 357  
 361 ILMEERFPRTLGPEAKSLGLKKDKPKQRLGGGSDAKETIMOHRRFAGIYVQHVYK 420  
 358 ILMEERFPRTLGPEAKSLGLKKDKPKQRLGGGSDAKETIMOHRRFAGIYVQHVYDK 417  
 421 LSPFPKQVTSFDTFYDEEFTAQMITITPPDQ--DDSMCEVDSERRPFPQFSYSASG 478  
 418 LVPFPKQVTSFDTFYDEEFTAQMITITPPDQ--DDSMCEVDSERRPFPQFSYSASG 477

RESULT 9

Tl7287

protein kinase (EC 2.7.1.37) akt3 short splice form - human  
 N:Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
 C:Accession: Tl7287  
 R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, September 1999  
 A:Reference number: 218723  
 A:Accession: Tl7287  
 A:Molecule type: mRNA  
 A:Residues: 1-462 <POU>  
 A:Cross-references: EMBL:AL117525; GB:CAB55977; NID:g5912043; PIDN:CAB55977.1  
 A:Experimental source: adult testis; clone DXF2p434N0250  
 R:Nakatani, K.; Thompson, D.A.; Barthel, A.; Sakaue, H.; Liu, W.; Weigel, R.J.; Roth, R.  
 J. Biol. Chem. 274, 21528-21532, 1999  
 A:Title: Up-regulation of Akt3 in estrogen receptor-deficient breast cancers and andrpg  
 A:Reference number: A64199; PMID:10419456  
 A:Contents: annotation  
 C:Comment: This protein is increased in estrogen receptor-negative breast cancers and an  
 C:Genetics:  
 A:Gene: GDB:AKT3  
 A:Cross-references: GDB:9954867  
 A:Map position: lq44-lq44  
 C:Function:  
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
 A:Pathway: signal transduction pathways regulating various processes  
 C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
 C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene



Db 107 VVKEGWLKRCGEHIKNWRQRFVVLHSDGLMGVRSKP--ADSASTPSPDFLLANNFTRGCQ 164  
Qy 62 LMKTERPRNPFTIIRCLQWTTVIERTHVTPEPEREWTTAIQTVADGLKKQBEEMDFR 121  
Db 165 IMTVDRPKPFTFIIRGLQWTTVIERTHVTPEPEREWTTAIRNVSSRLIDVGSVAM-- 221  
Qy 122 SGSPDSNGBAEMEV-SLAKPK-----HRVTNPEYLLKCKGTGK 163  
Db 222 --TPSEQTMDTVDVMTAIDELSEQFSVOQTTNCSGKVKVTLNPFELKVLGKGTGK 279  
Qy 164 VILVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALYSFQTHDRL 223  
Db 280 VILCRKATAKLYAIIKILKKEVILQKDEVAHTLTESRVKLTNPFLISLKYSFQTHDRL 339  
Qy 224 CFVMEYANGBELPHLSRVSFSDRARFYGAETVSALDYHLSKKNVYRDLKLENLMD 283  
Db 340 CFVQYVNGGELFWHLHERIFTEDRTRFYGAETISALGYLHSQ-GIIYRDLKLENLLD 398  
Qy 284 KDGHIKIDFGLCCKEGIKDGTMTFCGTPYLAPLEVLNDYDGRAVDWGLGVVYEMM 343  
Db 399 KDGHIKIDFGLCCKEDITYGRTTKTFCGTPYLAPLEVLNDYDQAVDWMGTGVVYEMI 458  
Qy 344 CGRLPFYNQDHEKLFELILMBEIRPRTLGPPEAKSLLSGLLKDPKORLGGSGSDAKEIM 403  
Db 459 CGRLPFYNRHDVLFLLVVEEVKFRNITDEAKNLLAGLLAKDPKRLGGGKDDVKEIQ 518  
Qy 404 QHRRFAGIVQHVVEKLSPPFPKQVTSQVSEDTTRYFDEFTAQMTITPPDODDSMECVDS 463  
Db 519 AHPFFASINWDLVLKIPPPKQVTSQVSEDTTRYFDEFTGESVELTPDPTGPLGSIAE 578  
Qy 464 ERHPFPQFSV-----SASGTA 480  
Db 579 E-PLFFPQFSYQGMMASTLGTGS 598

RESULT 12  
T43232  
Protein kinase (EC 2.7.1.37) akt-1 splice form b [similarity] - Caenorhabditis elegans  
N;Alternate names: PKB; protein kinase B  
C;Species: Caenorhabditis elegans  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: T43232; T19222  
R;Paradis, S.; Ruvkun, G.  
Genes Dev. 12, 2488-2498, 1998  
A;Title: Caenorhabditis elegans Akt/PKB transduces insulin receptor-like signals from AG  
A;Reference number: 222355; MUID:98382502; PMID:9716402  
A;Accession: T43232  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-546 <PAR>  
A;Cross-references: UNIPROT:Q17942; EMBL:AF072380; NID:g3694830; PIDN:AAC62467.1; PID:g3  
submitted to the EMBL Data Library, June 1996  
A;Reference number: 219092  
A;Accession: T19222  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-546 <WIL>  
A;Cross-references: EMBL:Z73969; PIDN:CAA98238.1; GSPDB:GNO0023; CESP:C12D8.10b  
A;Experimental source: clone C12D8  
C;Genetics:  
A;Gene: akt-1; C12D8.10  
A;Map position: 5  
A;Introns: 35/2; 71/3; 134/3; 188/3; 254/3; 323/3; 366/3; 487/3  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating metabolism, development, and longevity  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotrans  
F;14-116/Domain: pleckstrin repeat homology <PLK>  
F;191-455/Domain: protein kinase homology <KIN>  
F;199-207/Region: protein kinase ATP-binding motif  
F;222/Active site: Lys #status predicted

F;355/Binding site: phosphate (Thr) (covalent) #status predicted  
F;522/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 58.5%; Score 1490.5; DB 1; Length 546;  
Best Local Similarity 55.6%; Pred. No. 9.8e-57;  
Matches 283; Conservative 78; Mismatches 107; Indels 41; Gaps 7;

Qy 6 IVKEGWLKGEYIKTWPRFYFLKNDGTGTFYGERQDVVDQREAPLNNFSAQCQLMKT 65  
Db 16 WTIEGWLHKGEHIRNWRPFYFMINDGALGLGFAKPKGQFPPEPLNDFMKDAATMLF 75  
Qy 66 ERBPNTFIIRCLQWTTVIERTHVTPEPEREWTTAIQTVADGLK-----KQBE---- 115  
Db 76 EKRPANFWVRCLQWTTVIERTHVTFAESAERVQRWIIHAIESISKYKGTNANPQBELMETN 135  
Qy 116 -----EEMDFRS-----GSPDSNG-----AEMEVSLAKPKHRVTNPEY 152  
Db 136 QQPKIDEDSEFAGAAHAIMQPSGSGDNCSDIPRASMISIADTSEAAKRDKITMEDPDF 195  
Qy 153 LKLLCKGTGKVLIVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLQNSRHPFLTA 212  
Db 196 LKVLGKGTGKVLIVCKEKRTQKLYAIKILKQVIAAREEVAHTLTENRVLQRCXHPFLTE 255  
Qy 213 LKYSFQTHDRLCFVMEYANGGELFFHLRS-----RVFSEDRARFYGAETVSALDYHLS 267  
Db 256 LKYSFQTHDRLCFVMEYANGGELFFHLRS-----RVFSEDRARFYGAETVSALDYHLS 314  
Qy 268 KNVYRDLKLENLMDKDGHIKIDFGLCCKEGIKDGTMTFCGTPYLAPLEVLNDYD 327  
Db 315 NSIVYRDLKLENLLDKDGHKIDFGLCCKEISFGDKTSTFCGTPYLAPLEVLNDYD 374  
Qy 328 RAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMBEIRPRTLGPPEAKSLLSGLLKKD 387  
Db 375 RCVDWVGWGVVYEMMCGRLPFYKSKHKLKFLIMAGDLRFPSPKLSQEARLLTGLLVKD 434  
Qy 388 PKORLGGSGSDAKEIMOHRFPFAGIVQHVVEKLSPPFPKQVTSQVSEDTTRYFDEFTAQMI 447  
Db 435 PTKRLGGSGSDAKEIMOHRFPFAGIVQHVVEKLSPPFPKQVTSQVSEDTTRYFDEFTAQMI 494  
Qy 448 TITPPDODDSMECV--SERRPFPQFSY 474  
Db 495 QLTPSPSGALATVDEQEEMQSNFTQFSF 523

RESULT 13  
T43232  
Protein kinase (EC 2.7.1.37) akt-1 splice form a [similarity] - Caenorhabditis elegans  
N;Alternate names: PKB; protein kinase B  
C;Species: Caenorhabditis elegans  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: T43232; T19224  
R;Paradis, S.; Ruvkun, G.  
Genes Dev. 12, 2488-2498, 1998  
A;Title: Caenorhabditis elegans Akt/PKB transduces insulin receptor-like signals from AG  
A;Reference number: 222355; MUID:98382502; PMID:9716402  
A;Accession: T43232  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-541 <PAR>  
A;Cross-references: UNIPROT:Q17941; EMBL:AF072379; NID:g3694828; PIDN:AAC62466.1; PID:g3  
submitted to the EMBL Data Library, June 1996  
A;Reference number: 219092  
A;Accession: T19224  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-541 <WIL>  
A;Cross-references: EMBL:Z73969; PIDN:CAA98240.1; GSPDB:GNO0023; CESP:C12D8.10a  
A;Experimental source: clone C12D8  
C;Genetics:  
A;Gene: akt-1; C12D8.10  
A;Map position: 5  
A;Introns: 35/2; 71/3; 134/3; 188/3; 254/3; 318/3; 361/3; 482/3

C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating metabolism, development, and longevit  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotrans  
F;114-116/Domain: pleckstrin repeat homology <PLK>  
F;191-450/Domain: protein kinase ATP-binding motif  
F;199-207/Region: protein kinase ATP-binding motif  
F;222/Active site: Lys #status predicted  
F;350/Binding site: phosphate (Thr) (covalent) #status predicted  
F;517/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 57.6%; Score 1470; DB 1; Length 541;  
Best Local Similarity 55.4%; Pred. No. 7.2e-56;  
Matches 279; Conservative 75; Mismatches 114; Indels 36; Gaps 6;

Qy 6 IVKEGWLHKRGEYIKTWPRPYFLKNDGTFIGYKERPDVDQREAPLNFSVAQCQLMKT 65  
Db 16 VVIEGWLHKRGEHINRWPRPYFMFDGALLGFRPAKKEGQPPFPEPLNDFMIKDAATMLF 75  
Qy 66 ERPRNPTFIIRCLQWTTVIERTFHVETPEEREWTTAIQTVDGLK-----KQEE----- 115  
Db 76 EKPRPNFMVRCLOQWTTVIERTFVAESAERVQRWIHAIESISKYKGTNANPQBELMETN 135  
Qy 116 -----EEMDFRS-----GSPSDNSG-----AEMEVS LAKPHRVTMNEFEY 152  
Db 136 QQPKIDEDSEFAGAAHAIMGQSSGCHGDNCSIDFRASWISIADTSEAAKRDKITMEDFD 195  
Qy 153 LKLLGKGTGKVLIVKEKATGRYYAMKILKEVIVAKDEVAHTLTENRVLQNSHHPFLTA 212  
Db 196 LKVLGKGTGKVLIVKEKATGRYYAMKILKEVIVAKDEVAHTLTENRVLQNSHHPFLTA 255  
Qy 213 LKYSFQTHDLRCFVMEYANGGELFFHLRSRVRSEDRARFVGABIVSALDYLHSEKNVY 272  
Db 256 LKYSFQCHVLCFVMEYANGGELFFHLRSRVRSEDRARFVGABIVSALDYLHSEKNVY 314  
Qy 273 RDLKLEMLDKDGHIKITDFGLCKEGIKDGMATKTCGTPGYLAPEVLNDYGRAVDW 332  
Db 315 RDMKLEMLDKDGHIKITDFGLCKEGIKDGMATKTCGTPGYLAPEVLNDYGRAVDW 374  
Qy 333 WGLGVVMEYMCGLPPYNDQHEKLFELILMEEIRFPRTLGPEAKSLLSGLLKDPKQRL 392  
Db 375 WGVGVVMEYMCGLPPYNDQHEKLFELILMEEIRFPRTLGPEAKSLLSGLLKDPKQRL 434  
Qy 393 GGSSEDAKEIMQHRFFAGIVMHHVYKELGPPPKPQVTSSTDTTRYFDEEFTAQMITTPP 452  
Db 435 GGPEDALEICRADFFFTVDWEATYKAEIEPPYKPNVQSETDTSYFNDEFTSQPVQLTTP 494  
Qy 453 DQDDSMCEVD--SRRRPHFPQFSY 474  
Db 495 SRSGALATVDEQEEMQSNFTQFSF 518

RESULT 14  
T21523  
protein kinase (EC 2.7.1.37) akt-2 long splice form [similarity] - Caenorhabditis elegans  
N;Alternate names: PKB; protein kinase B  
C;Species: Caenorhabditis elegans  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: T21523; T23878  
R;McMurray, A.  
submitted to the EMBL Data Library, September 1998  
A;Reference number: Z19434  
A;Accession: T21523  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-528 <W1>  
A;Cross-references: UNIPROT:Q9XTG7; EMBL:AL031621; PIDN:CAA20936.1; GSPDB:GN00028; CESP:  
A;Experimental source: clone F28H6  
R;McMurray, A.  
submitted to the EMBL Data Library, March 1997  
A;Reference number: Z19812  
A;Accession: T23878

A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-528 <W12>  
A;Cross-references: EMBL:Z2837; PIDN:CAB07403.1; GSPDB:GN00028; CESP:F28H6.1  
A;Experimental source: clone R03E1  
C;Genetics:  
A;Gene: akt-2; CESP:F28H6.1  
A;Map position: X  
A;Introns: 32/2; 68/3; 135/3; 175/3; 241/3; 285/2; 305/3; 348/3; 469/3  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating metabolism, development, and longevit  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotrans  
F;11-113/Domain: pleckstrin repeat homology <PLK>  
F;178-437/Domain: protein kinase homology <KIN>  
F;186-194/Region: protein kinase ATP-binding motif  
F;209/Active site: Lys #status predicted  
F;337/Binding site: phosphate (Thr) (covalent) #status predicted  
F;505/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 54.5%; Score 1390.5; DB 1; Length 528;  
Best Local Similarity 52.7%; Pred. No. 1.7e-52;  
Matches 265; Conservative 87; Mismatches 118; Indels 33; Gaps 7;

Qy 6 IVKEGWLHKRGEYIKTWPRPYFLKNDGTFIGYKERPDVDQREAPLNFSVAQCQLMKT 65  
Db 13 IVIESWLHKRGEHINRWPRPYFILFRDGTLLGFRSPKEDQPLPEPLNNMIRDAATVCL 72  
Qy 66 ERPRNPTFIIRCLQWTTVIERTFHVETPEEREWTTAIQTVD-----GLKKQEE 117  
Db 73 DKPRPNMFIVRCLQWTTVIERTFVADSADPQMWIEAIAQVSSHNLKENAGNTSMQEE 132  
Qy 118 MDRFSQSPDSNSCA-----EEMEVS LAKP-----KRVTMNEFEVILKILGK 159  
Db 133 ---TNGNPSESDVNMNDATSTRSDNDFESTVMNIDPEEVPKNTVTMDDFDLKVLGQ 189  
Qy 160 TFGKVLIVKEKATGRYYAMKILKEVIVAKDEVAHTLTENRVLQNSHHPFLTALKYSFOT 219  
Db 190 TFGKVLIVKEKATGRYYAMKILKEVIVAKDEVAHTLTENRVLQNSHHPFLTALKYSFOT 249  
Qy 220 HDLRCFVMEYANGGELFFHLRSRVRSEDRARFVGABIVSALDYLHSEKNVYRDLEK 279  
Db 250 QYHICFVMEYANGGELFFHLRSRVRSEDRARFVGABIVSALDYLHSEKNVYRDLEK 308  
Qy 280 LMLDKDGHIKITDFGLCKEGIKDGMATKTCGTPGYLAPEVLNDYGRAVDWGLGVV 339  
Db 309 LLLDRDGHIKITDFGLCKEGIKDGMATKTCGTPGYLAPEVLNDYGRAVDWGLGVV 368  
Qy 340 YEMMCGRLPPYNDQHEKLFELILMEEIRFPRTLGPEAKSLLSGLLKDPKQRLGGGSEDA 399  
Db 369 YEMMCGRLPPYNDQHEKLFELILMEEIRFPRTLGPEAKSLLSGLLKDPKQRLGGGSEDA 428  
Qy 400 KEIMQHRFFAGIVMHHVYKELGPPPKPQVTSSTDTTRYFDEEFTAQMITTPDQDDSM 459  
Db 429 REVSRAEAFKVDWEATYKAEIEPPYKPNVQSETDTSYFNDEFTSQPVQLTTPP 488  
Qy 460 CVDSEK--RPHFPQF--SYSASGT 479  
Db 489 TVDEEBELQANFIQFASYYVSGS 511

RESULT 15  
T43234  
protein kinase (EC 2.7.1.37) akt-2 short splice form [similarity] - Caenorhabditis elegans  
N;Alternate names: PKB; protein kinase B  
C;Species: Caenorhabditis elegans  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: T43234  
R;Paradis, S.; Ruvkun, G.  
Genes Dev. 12, 2488-2496, 1998  
A;Title: Caenorhabditis elegans Akt/PKB transduces insulin receptor-like signals from AGI  
A;Reference number: Z22355; MUID:98382502; PMID:9716402

A:Accession: T43234  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-483 <PAR>  
A:Cross-references: UNIPROT:O77145; EMBL:AF072381; NID:g3694832; PIDN:AAC62468.1; PID:g3  
C:Genetics:  
A:Gene: akt-2  
C:Function:  
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A:Pathway: signal transduction pathways regulating metabolism, development, and longevi  
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C:Keywords: alternative splicing; ATP; phosphoprotein; phosphotransferase; serine/threon  
F:11-113/Domain: pleckstrin repeat homology <PLK>  
F:178-437/Domain: protein kinase homology <KIN>  
F:186-194/Region: protein kinase ATP-binding motif  
F:209/Active site: Lys #status predicted  
F:337/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 51.9%; Score 1324; DB 1; Length 483;  
Best Local Similarity 54.1%; Pred. No. 1e-49;  
Matches 249; Conservative 78; Mismatches 103; Indels 30; Gaps 5;

Qy 6 IVKEGWLHKGREYIKTWPRYFLKNDGTFYGYKERPOVDQREAPLNFSVAQCQLMKT 65  
Db 13 IVIESWLHKGGEHINRNPRIYFILFRDGTLLGFRSKPKEDQPLPEPLNPNIRDAATVCL 72

Qy 66 ERPRNPTIIRCLQWTTVIERTFHVETPEEREETTAQTAD-----GLKKQEEEE 117  
Db 73 DKPRNMFIVRCLQWTTVIERTFVADSADFRQMITEATQAVSSHNLKENAGNTSMQBED 132

Qy 118 MDRSGSPSDNSGA-----EEMEVSLAKP-----KRVVTMNEFEYLKLLGKG 159  
Db 133 ---TGNPFGSDVNM DATSTRSDNFSTVMNIDPEEVPKNTVTMTDDFDFLKLGGG 189

Qy 160 TFGKVLVKEKATGRYAMKILKKEVIKADDEVAHTLTENRVLQNSRHPFLTALKYSFQT 219  
Db 190 TFGKVLCKREKSKDKLYAKIKRMVVDREVAHTLTENRVLYACVHPFLTLLKYSFQA 249

Qy 220 HDRLCFVMEYANGGELPFHLGRVFSERDARFYGAETVSALDYHSEKNVYVYRDLEN 279  
Db 250 QYHICFVMEFANGGELFTHLQRCCKTFSEARTFYGSEIILALGYLH-HRNIVYRDMKLEN 308

Qy 280 LMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPYLAPEVLENDYGRAVDWMLGVVM 339  
Db 309 LLLDRDGHIKITDFGLCKEEIKYGDKTSTFCGTPYLAPEVIDIDYDRSDWMLGVVM 368

Qy 340 YEMMCGRLPFYQDHEKLFELILMBEIRFPRTLGLPEAKSLLSGLIKKDPKQRLGGGSDA 399  
Db 369 YEMMCGRLPFSAKENGKLFELITTCDLAKFPNRLSPEAVTLLSGLLERYVPKRLGAGPDDA 428

Qy 400 KEIMQHRPFAGIVQHVYEKLSPPFKQVTSFDTTRYFD 439  
Db 429 REVSRAEFPKDVMEATLRKEVEPPFKPNVMSFDTTSFFD 468

Search completed: February 23, 2005, 20:49:12  
Job time : 44 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 23, 2005, 20:22:18 ; Search time 164 Seconds  
(without alignments)  
1131.982 Million cell updates/sec

Title: US-10-621-485A-1  
Perfect score: 2550  
Sequence: 1 MSDVAIVKEGWLHKGVEYK.....VDSERRPHFQFSYASSTA 480

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04:.\*  
1: geneseqp1980s:.\*  
2: geneseqp1990s:.\*  
3: geneseqp2000s:.\*  
4: geneseqp2001s:.\*  
5: geneseqp2002s:.\*  
6: geneseqp2003as:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 2550  | 100.0       | 492    | ABO27207 | ABO27207 Human sig |
| 2          | 2544  | 99.8        | 480    | AAW17972 | AAW17972 Human RAC |
| 3          | 2544  | 99.8        | 480    | AAW18515 | AAW18515 Human RAC |
| 4          | 2544  | 99.8        | 480    | AAW52706 | AAW52706 Human AKT |
| 5          | 2544  | 99.8        | 480    | AAW33999 | AAW33999 Human AKT |
| 6          | 2544  | 99.8        | 480    | ADP77614 | ADP77614 Human AKT |
| 7          | 2544  | 99.8        | 480    | AAW92221 | AAW92221 Wild type |
| 8          | 2544  | 99.8        | 480    | AAW78020 | AAW78020 Human AKT |
| 9          | 2544  | 99.8        | 480    | AAW67620 | AAW67620 Amino aci |
| 10         | 2544  | 99.8        | 480    | AAW67441 | AAW67441 Amino aci |
| 11         | 2544  | 99.8        | 480    | AAW79418 | AAW79418 Human pro |
| 12         | 2544  | 99.8        | 480    | AAW17782 | AAW17782 Human AKT |
| 13         | 2544  | 99.8        | 480    | ABW06996 | ABW06996 Human AKT |
| 14         | 2544  | 99.8        | 480    | ABW57472 | ABW57472 Human PKB |
| 15         | 2544  | 99.8        | 480    | ADP18630 | ADP18630 Human AKT |
| 16         | 2544  | 99.8        | 480    | ADP45032 | ADP45032 Human kin |
| 17         | 2544  | 99.8        | 480    | ADL25355 | ADL25355 Human ARK |
| 18         | 2544  | 99.8        | 480    | ADQ22518 | ADQ22518 Biochemic |
| 19         | 2544  | 99.8        | 480    | ADQ37844 | ADQ37844 Human pro |
| 20         | 2544  | 99.8        | 480    | ADQ06338 | ADQ06338 IRK-1 pro |
| 21         | 2544  | 99.8        | 480    | ABW81592 | ABW81592 Tumour-as |
| 22         | 2544  | 99.8        | 480    | ADQ31934 | ADQ31934 Human wil |
| 23         | 2544  | 99.8        | 524    | ADM24838 | ADM24838 Human AKT |
| 24         | 2544  | 99.8        | 524    | ADM24838 | ADM24838 Human AKT |
| 25         | 2544  | 99.8        | 726    | AAW85022 | AAW85022 PKB-green |
| 26         | 2544  | 99.8        | 727    | AAW85041 | AAW85041 Green flu |

|    |        |      |     |   |          |                    |
|----|--------|------|-----|---|----------|--------------------|
| 26 | 2540   | 99.6 | 480 | 2 | AAW17984 | AAW17984 Human RAC |
| 27 | 2538   | 99.5 | 480 | 2 | AAW17983 | AAW17983 Human RAC |
| 28 | 2534   | 99.4 | 480 | 2 | AAW17985 | AAW17985 Human RAC |
| 29 | 2509   | 98.4 | 480 | 3 | AAW92223 | AAW92223 Wild type |
| 30 | 2509   | 98.4 | 480 | 5 | AAE17784 | AAE17784 Mouse Akt |
| 31 | 2509   | 98.4 | 501 | 2 | AAW03452 | AAW03452 Mouse v-A |
| 32 | 2509   | 98.4 | 517 | 8 | ADL25357 | ADL25357 ARK5 rela |
| 33 | 2503   | 98.2 | 480 | 7 | ADW83507 | ADW83507 Rat Prote |
| 34 | 2494   | 97.8 | 480 | 3 | AAW06176 | AAW06176 Human hAK |
| 35 | 2493.5 | 97.8 | 479 | 2 | AAW03453 | AAW03453 Mouse c-A |
| 36 | 2464   | 96.6 | 480 | 8 | ADN71942 | ADN71942 Chicken s |
| 37 | 2161.5 | 84.8 | 417 | 3 | AAW92222 | AAW92222 Partial w |
| 38 | 2161.5 | 84.8 | 417 | 5 | AAE17783 | AAE17783 Human Akt |
| 39 | 2156.5 | 84.6 | 417 | 8 | ADO55980 | ADO55980 Human Akt |
| 40 | 2138.5 | 83.5 | 488 | 8 | ABO84895 | ABO84895 Murine ca |
| 41 | 2126.5 | 83.4 | 480 | 4 | AAW78019 | AAW78019 Human Akt |
| 42 | 2126.5 | 83.4 | 480 | 4 | AAW19997 | AAW19997 Human ser |
| 43 | 2126.5 | 83.4 | 480 | 8 | ADG85254 | ADG85254 Human Chr |
| 44 | 2126.5 | 83.4 | 481 | 3 | AAW53246 | AAW53246 Human Akt |
| 45 | 2126.5 | 83.4 | 481 | 5 | AAW79419 | AAW79419 Human pro |

## ALIGNMENTS

RESULT 1  
ABO27207  
ID ABO27207 standard; protein; 492 AA.  
XX ABO27207;  
AC  
XX  
DT 10-SEP-2003 (first entry)  
DE Human signal transduction pathway component HJBCX80.  
XX  
KW Human; signal transduction pathway component; gene therapy; cancer;  
KW neural disorder; immune system disorder; systemic lupus erythematosus;  
KW rheumatoid arthritis; multiple sclerosis; muscular disorder; sinusitis;  
KW respiratory disease; nasal vestibulitis; nasal polyp; pulmonary disorder;  
KW cardiovascular disorder; congenital heart defect; Ebstein's anomaly;  
KW hypoplastic left heart syndrome; renal disorder; acute kidney failure;  
KW end-stage renal disease; hyperproliferative disorder; Hodgkin's disease;  
KW leukaemia; inflammatory disease; septic shock; bursitis; appendicitis;  
KW allergy; asthma; blood related disorder; thrombosis; atherosclerosis;  
KW myocardial infarction; endocrine disorder; Addison's disease; dysphagia;  
KW corticosteroid deficiency; reproductive system disorder; dysmenorrhea;  
KW testicular atrophy; gastrointestinal disorder; irritable bowel syndrome;  
KW infectious disease; wound healing; epithelial cell proliferation.

XX Homo sapiens.  
OS US2003036505-A1.  
XX  
XX US2003036505-A1.  
XX  
XX 20-FEB-2003.  
XX  
XX 20-SEP-2001; 2001US-009555999.  
XX  
XX 25-SEP-2000; 2000US-0234997P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Barash SC, Ni J, Ruben SM, Rosen CA, Young PE, Rohrschneider LR;  
XX WPI; 2003-492122/46.  
XX N-PSDB; ACD44893.  
XX  
XX New isolated nucleic acids encoding signal transduction pathway component  
XX polypeptides, useful for diagnosing, treating, and/or preventing  
XX disorders, such as cancer, infections, cardiovascular and inflammatory  
XX diseases.  
XX  
XX Claim 11; Page 270-271; 297pp; English.

CC The invention relates to an isolated nucleic acid molecule. The methods  
 CC and compositions of the present invention are useful for diagnosing,  
 CC treating, preventing and/or prognosing disorders related to the novel  
 CC polypeptides, such as neural disorders, immune system disorders (e.g.  
 CC systemic lupus erythematosus, rheumatoid arthritis, or multiple  
 CC sclerosis), muscular disorders, respiratory diseases (e.g. nasal  
 CC vestibulitis, nasal polyps, or sinusitis), reproductive disorders,  
 CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders  
 CC (e.g. congenital heart defects, Ebstein's anomaly or hypoplastic left  
 CC heart syndrome), renal disorders (e.g. acute kidney failure, or end-stage  
 CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease or  
 CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis, or  
 CC appendicitis), allergic reactions and conditions (e.g. asthma), blood  
 CC related disorders (e.g. thrombosis, atherosclerosis or myocardial  
 CC infarction), endocrine disorders (e.g. Addison's disease or  
 CC corticosteroid deficiency), reproductive system disorders (e.g.  
 CC testicular atrophy or dysmenorrhea), gastrointestinal disorders (e.g.  
 CC dysphagia or irritable bowel syndrome), infectious diseases, and/or  
 CC cancerous diseases. The polynucleotides can also be used to aid wound  
 CC healing and epithelial cell proliferation. The present sequence  
 CC represents the amino acid sequence of a human signal transduction pathway  
 CC component  
 XX  
 SQ Sequence 492 AA;

Query Match 100.0%; Score 2550; DB 6; Length 492;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-235;  
 Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MSDVAIVKEGWLHKGRIYIKTWPRYFLKNDGTFIGYKRPQDVQREAPLNFSVAQC 60  
 Db 13 MSDVAIVKEGWLHKGRIYIKTWPRYFLKNDGTFIGYKRPQDVQREAPLNFSVAQC 72  
 Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAQTVDGLKQEEEMDF 120  
 Db 73 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAQTVDGLKQEEEMDF 132  
 Qy 121 RSGSPDSNGAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYAMKI 180  
 Db 133 RSGSPDSNGAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYAMKI 192  
 Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFPFHL 240  
 Db 193 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFPFHL 252  
 Qy 241 RERVESDRARFYGAIEVSALDYLHSEKNVYVYRDILKLENMLDKDGHIKITDFGLCKEGI 300  
 Db 253 RERVESDRARFYGAIEVSALDYLHSEKNVYVYRDILKLENMLDKDGHIKITDFGLCKEGI 312  
 Qy 301 KDGATMTKTCGTPPEYLAPEVLEDNDYGRAVDWGLGVVMYEMMCGRLPFYVQDHEKLFEL 360  
 Db 313 KDGATMTKTCGTPPEYLAPEVLEDNDYGRAVDWGLGVVMYEMMCGRLPFYVQDHEKLFEL 372  
 Qy 361 ILMEERFPRTLGPPEAKSLLSGLLKQPKQRLGGSEDAKEIMQHRFFAGIVMHHVYVEKK 420  
 Db 373 ILMEERFPRTLGPPEAKSLLSGLLKQPKQRLGGSEDAKEIMQHRFFAGIVMHHVYVEKK 432  
 Qy 421 LSPFPKQVTSSETTRFDEEFTAQMITTPPDQDSDMECVDSRRRPHFPQFSYASGTA 480  
 Db 433 LSPFPKQVTSSETTRFDEEFTAQMITTPPDQDSDMECVDSRRRPHFPQFSYASGTA 492

RESULT 2

AAW17972  
 ID AAW17972 standard; protein; 480 AA.  
 XX  
 AC AAW17972;  
 XX  
 DT 12-DEC-1997 (first entry)  
 XX  
 DE Human RAC protein kinase alpha.  
 XX  
 KW RAC protein kinase C-terminal binding protein; CTBP; modulator;

KW signal transduction; insulin; diabetes; cell proliferation; glycogen;  
 KW therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9718303-A1.  
 XX  
 PD 22-MAY-1997.  
 XX  
 PF 05-NOV-1996; 96WO-EP004810.  
 XX  
 PR 16-NOV-1995; 95GB-00023379.  
 PR 15-DEC-1995; 95GB-00025704.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 XX  
 PI Hemmings BA;  
 XX  
 DR WPI; 1997-289279/26.  
 DR N-PSDB; AAT67135.  
 XX  
 PT RAC protein kinase, or modulator excluding wortmannin and vanadate, for  
 PT use as medicament - and screening potential modulators of insulin  
 PT mediated intracellular signalling using RAC-PK, or fragment.  
 XX  
 PS Claim 1; Page 30-32; 38pp; English.  
 XX  
 CC This polypeptide sequence comprises human RAC protein kinase alpha (RAC-  
 CC PK), a protein directly involved in the inactivation of glycogen  
 CC synthetase kinase-3 and the activation of IMP dehydrogenase and in the  
 CC regulation of insulin-dependent signalling pathways, which control  
 CC cellular proliferation. RAC-PK and its fragments and modulators are  
 CC claimed for use as medicaments for the treatment of diseases involving  
 CC abnormalities in processes modulated by insulin, such as cellular  
 CC proliferation, insulin deficiency and/or excess blood sugar levels. RAC-  
 CC PK can also be used in a claimed method for screening potential  
 CC modulators of insulin-mediated intracellular signalling. Activated mutant  
 CC RAC-PKs (see AAW17983-85) may also be used in such screenings  
 XX  
 SQ Sequence 480 AA;

Query Match 99.8%; Score 2544; DB 2; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGRIYIKTWPRYFLKNDGTFIGYKRPQDVQREAPLNFSVAQC 60  
 Db 1 MSDVAIVKEGWLHKGRIYIKTWPRYFLKNDGTFIGYKRPQDVQREAPLNFSVAQC 60  
 Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAQTVDGLKQEEEMDF 120  
 Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAQTVDGLKQEEEMDF 120  
 Qy 121 RSGSPDSNGAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYAMKI 180  
 Db 121 RSGSPDSNGAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYAMKI 180  
 Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFPFHL 240  
 Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFPFHL 240  
 Qy 241 RERVESDRARFYGAIEVSALDYLHSEKNVYVYRDILKLENMLDKDGHIKITDFGLCKEGI 300  
 Db 241 RERVESDRARFYGAIEVSALDYLHSEKNVYVYRDILKLENMLDKDGHIKITDFGLCKEGI 300  
 Qy 301 KDGATMTKTCGTPPEYLAPEVLEDNDYGRAVDWGLGVVMYEMMCGRLPFYVQDHEKLFEL 360  
 Db 301 KDGATMTKTCGTPPEYLAPEVLEDNDYGRAVDWGLGVVMYEMMCGRLPFYVQDHEKLFEL 360  
 Qy 361 ILMEERFPRTLGPPEAKSLLSGLLKQPKQRLGGSEDAKEIMQHRFFAGIVMHHVYVEKK 420  
 Db 361 ILMEERFPRTLGPPEAKSLLSGLLKQPKQRLGGSEDAKEIMQHRFFAGIVMHHVYVEKK 420

QY 421 LSPPPKQVTSSTDRYDFDEFTAQMITTPDQDDSMCEVDSERRPHFPQPSYASGTA 480  
 DB 421 LSPPPKQVTSSTDRYDFDEFTAQMITTPDQDDSMCEVDSERRPHFPQPSYASGTA 480

RESULT 3  
 AAW18515  
 ID AAW18515 standard; protein; 480 AA.  
 XX AAW18515;  
 XX AAW18515;  
 DT 16-FEB-1998 (first entry)  
 DE Human RAC protein kinase alpha.  
 XX RAC protein kinase; pleckstrin homology domain; signal modulator;  
 KW screening; fluorescence; human.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FT Misc-difference 22  
 FT /note= "fluorescence is associated with the Trp-22  
 FT residue"  
 XX W09722717-A1.  
 XX 26-JUN-1997.  
 XX 05-NOV-1996; 96WO-EP004814.  
 PR 15-DEC-1995; 95GB-00025703.  
 PR 15-DEC-1995; 95GB-00025705.  
 XX (NOVS ) NOVARTIS AG.  
 XX Hemmings BA, Frech M;  
 XX WPI; 1997-341705/31.  
 DR N-PSDB; AAT64812.

Screening for modulators of signal pathways - by incubation with  
 fluorescently labelled pleckstrin homology domain of signalling molecule  
 and detecting changes in fluorescence.

Disclosure; Page 16-19; 39pp; English.

This protein comprises human RAC protein kinase. The N-terminal  
 pleckstrin homology (PH) domain of RAC protein kinase can be used in a  
 claimed method for screening for modulators of signal pathways. This  
 involves: (a) incubating the test compound with the PH domain of a  
 signalling molecule which is capable of fluorescing; and (b) determining  
 phospholipid-induced changes in fluorescence, indicating a functional  
 interaction between the compound and the PH domain. Fluorescence is  
 preferably associated with the Trp-223 of RAC protein kinase PH domain.  
 The method allows screening for compounds which modulate signal pathways  
 involving the serine/threonine kinase RAC and can especially be applied  
 to protein kinases and their substrates, which are implicated in  
 intracellular signalling and growth control. The high affinity binding of  
 phospholipid to the PH domain of signalling molecules suggests that this  
 domain is a membrane anchor for the molecules; molecule interactions with  
 the cell membrane are important for their stable interaction with  
 membrane-bound partners in signalling pathways, so that disruption of the  
 interaction modulates the signalling effect. By measuring this modulation  
 (which may be down-regulation for stimulatory interactions or  
 upregulation for inhibitory interactions) compounds which can have an  
 effect can be identified e.g. agents which cause conformational changes  
 in the PH domains or which compete directly for binding of the PH domain  
 to the cell membrane. A claimed method for production of the RAC protein  
 kinase PH domain in a bacterial cell comprises expressing a nucleic acid  
 sequence encoding the PH domain having at least 3 hydrophilic amino acids  
 (preferably lys) residues joined directly at its C-terminus (see  
 AAW18515)

XX Sequence 480 AA;  
 SQ Query Match 99.8%; Score 2544; DB 2; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MSDVAIVKEGWLHKRGEYIKTRPRYFLLLKNDGTFIGYKERPDQVDOREAPLNNSVAQC 60  
 DB 1 MSDVAIVKEGWLHKRGEYIKTRPRYFLLLKNDGTFIGYKERPDQVDOREAPLNNSVAQC 60  
 QY 61 QLMKTERPRNPTFIIRCLQWTTVIERTPHVTPEEREEMTTAIQTVAOGLKKQSEEMDF 120  
 DB 61 QLMKTERPRNPTFIIRCLQWTTVIERTPHVTPEEREEMTTAIQTVAOGLKKQSEEMDF 120  
 QY 121 RSGSPDSNGAEEMEVSLAKPKHRTVMEFEYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
 DB 121 RSGSPDSNGAEEMEVSLAKPKHRTVMEFEYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
 QY 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFWMYANGGELFFHLS 240  
 DB 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFWMYANGGELFFHLS 240  
 QY 241 RERVSEDRARFYGAEIVSALDYLSHSEKVVVYRDLLKLENMLDKDGHKIKITDFGLCKEGI 300  
 DB 241 RERVSEDRARFYGAEIVSALDYLSHSEKVVVYRDLLKLENMLDKDGHKIKITDFGLCKEGI 300  
 QY 301 KDGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYQDHEKLFEL 360  
 DB 301 KDGATMTKTCGTPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYQDHEKLFEL 360  
 QY 361 ILMBEIRPPRTLGPPEAKSLLSGLLKQDKQRLGGGSEDAKEIMQHRFPAGIVQHVYKXK 420  
 DB 361 ILMBEIRPPRTLGPPEAKSLLSGLLKQDKQRLGGGSEDAKEIMQHRFPAGIVQHVYKXK 420  
 QY 421 LSPBPKQVTSSTDRYDFDEFTAQMITTPDQDDSMCEVDSERRPHFPQPSYASGTA 480  
 DB 421 LSPBPKQVTSSTDRYDFDEFTAQMITTPDQDDSMCEVDSERRPHFPQPSYASGTA 480

RESULT 4  
 AAY52706  
 ID AAY52706 standard; protein; 480 AA.  
 XX AAY52706;  
 XX AAY52706;  
 DT 26-JAN-2000 (first entry)  
 DE Human AKT-1 protein.  
 XX Identification; genetic target; gene modulation; human;  
 KW antisense oligonucleotide; phosphorothioate; target validation;  
 KW nucleotide sequence-based technology; antisense drug discovery.  
 XX Homo sapiens.  
 OS WO9953101-A1.  
 PN 21-OCT-1999.  
 PD 13-APR-1999; 99WO-US008268.  
 PR 13-APR-1998; 98US-0081483P.  
 PR 28-APR-1998; 98US-00067638.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Cowsext LM, Baker BF, Mcneil J, Freier SM, Saamor HM, Brooks DG;  
 PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;  
 XX WPI; 1999-620446/53.  
 DR N-PSDB; AAZ41177.

PT Identifying compounds which modulate expression of nucleic acids, used to  
 PT provide compounds having defined physical, chemical or bioactive  
 PS properties, e.g. antisense activity.

XX Example 29; Page 248-251; 264pp; English.

CC A method has been developed of defining a set of compounds that modulate  
 CC the expression of a target nucleic acid (tNA) sequence via binding of the  
 CC compounds with the tNA sequence. The method comprises generating a  
 CC library of virtual compounds in silico according to defined criteria, and  
 CC evaluating in silico the binding of the virtual compounds with the tNA  
 CC according to defined criteria. Also described are: (1) a method of  
 CC defining a set of oligonucleotides (ONs) that modulate the expression of  
 CC a tNA sequence via binding of the ONs with the tNA sequence comprising  
 CC generating a library of virtual compounds in silico according to defined  
 CC criteria, and evaluating in silico the binding of the virtual ONs with  
 CC the tNA according to defined criteria; and (2) a method of defining a set  
 CC of compounds that modulate the expression of a tNA sequence via binding  
 CC of the compounds with the tNA. The methods can be used for the generation  
 CC and identification of synthetic compounds having defined physical,  
 CC chemical or bioactive properties. Information gathered from assays of  
 CC such compounds is used to identify nucleic acid sequences that are  
 CC tractable to a variety of nucleotide sequence-based technologies, e.g.  
 CC antisense drug discovery and target validation. AA240852 to AA241220, and  
 CC AAY52701 to AAY52706, represent sequences used in the exemplification of  
 CC the present invention

XX Sequence 480 AA;

Query Match 99.8%; Score 2544; DB 2; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLKRGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60  
 Db 1 MSDVAIVKEGWLKRGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60  
 Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEREEWTTAQTVDAGLKKQEEBEMDF 120  
 Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEREEWTTAQTVDAGLKKQEEBEMDF 120  
 Qy 121 RSGSPSDNSGAEEMVSLAKPKHRTVMNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
 Db 121 RSGSPSDNSGAEEMVSLAKPKHRTVMNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
 Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGSELPFHL 240  
 Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGSELPFHL 240  
 Qy 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDFGLCKEGI 300  
 Db 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDFGLCKEGI 300  
 Qy 301 KDGMTKTCFCTPEYLAPEVLENDYGRAVDWGLGVVMYEMMCGRLPFYVQDHEKLFEL 360  
 Db 301 KDGMTKTCFCTPEYLAPEVLENDYGRAVDWGLGVVMYEMMCGRLPFYVQDHEKLFEL 360  
 Qy 361 ILMEIIRFPRTLGPPEAKSLLSGLLKDPKQRLGGSEDAKEIMQHRFFAGIVMHOVYVEKK 420  
 Db 361 ILMEIIRFPRTLGPPEAKSLLSGLLKDPKQRLGGSEDAKEIMQHRFFAGIVMHOVYVEKK 420  
 Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRPHFPQFSYASSTA 480  
 Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRPHFPQFSYASSTA 480

RESULT 5

AA33999

ID AA33999 standard; protein; 480 AA.

XX AA33999;

AC AA33999;

XX DT 26-NOV-1999 (first entry)

XX Human Akt-1 protein sequence.  
 DB Human; Akt-1; antisense; diagnostic; therapeutic; prophylaxis; infection;  
 KW inflammation; tumor formation.  
 XX Homo sapiens.

XX US5958773-A.

XX 28-SEP-1999.

XX 17-DEC-1998; 98US-00212771.

XX 17-DEC-1998; 98US-00212771.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Cowser LM;

XX WPI; 1999-561048/47.

XX N-PSDB; AA222190.

XX Antisense compounds complementary to Akt-1 useful for, e.g. diagnostics,  
 PT therapeutics and as research reagents.  
 XX Example 13; Col 43-46; 32pp; English.

XX The invention provides antisense compounds of 8-30 nucleotides that  
 CC inhibit the expression of human Akt-1. The antisense compounds may be  
 CC used for diagnostics, therapeutics (for modulating the expression of Akt-  
 CC 1), prophylaxis (e.g. to prevent or delay infection, inflammation, or  
 CC tumor formation), as research reagents (e.g. to distinguish between  
 CC members of a biological pathway) and in kits. The present sequence  
 CC represents the human Akt-1 protein sequence

XX Sequence 480 AA;

Query Match 99.8%; Score 2544; DB 2; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLKRGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60  
 Db 1 MSDVAIVKEGWLKRGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60  
 Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEREEWTTAQTVDAGLKKQEEBEMDF 120  
 Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEREEWTTAQTVDAGLKKQEEBEMDF 120  
 Qy 121 RSGSPSDNSGAEEMVSLAKPKHRTVMNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
 Db 121 RSGSPSDNSGAEEMVSLAKPKHRTVMNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
 Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGSELPFHL 240  
 Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGSELPFHL 240  
 Qy 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDFGLCKEGI 300  
 Db 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDFGLCKEGI 300  
 Qy 301 KDGMTKTCFCTPEYLAPEVLENDYGRAVDWGLGVVMYEMMCGRLPFYVQDHEKLFEL 360  
 Db 301 KDGMTKTCFCTPEYLAPEVLENDYGRAVDWGLGVVMYEMMCGRLPFYVQDHEKLFEL 360  
 Qy 361 ILMEIIRFPRTLGPPEAKSLLSGLLKDPKQRLGGSEDAKEIMQHRFFAGIVMHOVYVEKK 420  
 Db 361 ILMEIIRFPRTLGPPEAKSLLSGLLKDPKQRLGGSEDAKEIMQHRFFAGIVMHOVYVEKK 420  
 Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRPHFPQFSYASSTA 480  
 Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRPHFPQFSYASSTA 480



CC It is therefore also useful for treating muscular dystrophy, spinal  
 CC muscular atrophy, anabolic steroid-induced muscle injury, skeletal muscle  
 CC oxidative stress, physical exercise and unloading-induced skeletal muscle  
 CC atrophy. The Akt protein can also be used in screening for an inhibitory  
 CC agent that inhibits apoptotic cell-death of cells  
 XX  
 SQ Sequence 480 AA;

Query Match 99.8%; Score 2544; DB 3; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFYGYKRPQDVQREAPLNFSVAQC 60  
 Db 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFYGYKRPQDVQREAPLNFSVAQC 60  
 Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREWTATQTVADGLKQEEEMDF 120  
 Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREWTATQTVADGLKQEEEMDF 120  
 Qy 121 RSGSPDSNGAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
 Db 121 RSGSPDSNGAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
 Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELPFHLS 240  
 Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELPFHLS 240  
 Qy 241 RERFSEDRAFYGAETVSALDYHSEKNVYRDLENLMDKDGHIKITDGLCKEGI 300  
 Db 241 RERFSEDRAFYGAETVSALDYHSEKNVYRDLENLMDKDGHIKITDGLCKEGI 300  
 Qy 301 KDGATMTFCGTPPYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
 Db 301 KDGATMTFCGTPPYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
 Qy 361 ILMEIIRFPRTLGPPEAKSLLSGLLKDPKQRLGGSEDAKEIMQHRFFAGIVQHVEYKK 420  
 Db 361 ILMEIIRFPRTLGPPEAKSLLSGLLKDPKQRLGGSEDAKEIMQHRFFAGIVQHVEYKK 420  
 Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDDDSMECVDSERRPHFPQFSYASGTA 480  
 Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDDDSMECVDSERRPHFPQFSYASSTA 480

RESULT 8  
 AAG78020  
 ID AAG78020 standard; protein; 480 AA.  
 XX AC AAG78020;  
 XX DT 31-JAN-2002 (first entry)  
 XX DE Human Akt1.  
 XX KW Human; Akt3; AH/PH-domain containing serine/threonine kinase; Akt;  
 KW cerebroprotective; neurotrophic; hepatotrophic; inhibitor of apoptosis; ASK1;  
 KW osteopathic; vasotrophic; hepatotrophic; inhibitor of apoptosis; ASK1;  
 KW apoptosis stimulating kinase 1; hypoxia; necrosis; myocardial infarction;  
 KW ischaemia reperfusion injury; stroke; organ transplantation;  
 KW coronary artery bypass; tumour cell survival; gene therapy;  
 KW Alzheimer's disease; osteoarthritis; Akt1.  
 XX OS Homo sapiens.  
 XX PN W0200168850-A2.  
 XX PD 20-SEP-2001.  
 XX PF 09-MAR-2001; 2001WO-US007663.  
 XX PR 14-MAR-2000; 2000US-00526043.

PA (AVET ) AVENTIS PHARM PROD INC.  
 XX Guo K, Pagnoni MF, Clark XL, Ivashchenko YD;  
 XX WPI; 2001-582452/65.  
 XX New nucleic acid encoding human Akt3 protein, useful for inhibiting cell  
 PT death and treating myocardial infarction, ischemia reperfusion injury  
 PT associated with stroke, liver damage and renal failure.  
 XX  
 PS Example 1; Fig 1; 73pp; English.

CC The invention relates to human Akt3 protein (AH/PH-domain containing  
 CC serine/threonine kinase, Akt) comprising a fully defined sequence  
 CC (AAG78018) of 465 amino acids, its splice variant or allelic variant,  
 CC where the encoding polynucleotide hybridizes under stringent conditions  
 CC with a nucleic acid containing a nucleotide sequence (AAH78025) of 1570  
 CC base pairs defined in the specification. Akt3 has cerebroprotective,  
 CC hepatotrophic activity, as an inhibitor of apoptosis and/or apoptosis  
 CC stimulating kinase 1 (ASK1)-induced cell death. Akt3 operably linked to a  
 CC regulatory region is useful for inhibiting cell death in cardiac myocytes  
 CC resulting from hypoxia, apoptosis or necrosis and for treating myocardial  
 CC infarction or ischaemia reperfusion injury, particularly that associated  
 CC with stroke, liver damage, renal failure, organ transplantation or  
 CC coronary artery bypass grafting. Agonist of Akt3 are useful for improving  
 CC Akt3 activity during treatment of patients suffering from myocardial  
 CC infarction or ischaemia reperfusion injury and inhibitors of Akt3  
 CC activity decrease tumour cell survival and result in tumour regression.  
 CC Akt3 protects cells from apoptosis. Gene therapy using Akt3 reduces the  
 CC quantity of cell death and final infarct size, resulting in improved post  
 CC -infarction function, improved quality of life and reduced mortality. In  
 CC patients with existing heart failure, gene therapy with Akt3 retards the  
 CC process of ventricular dilation and slows down disease progression. Akt3  
 CC gene therapy is useful for treating other disease states, involving cell  
 CC death by apoptosis, including Alzheimer's disease, liver degeneration or  
 CC osteoarthritis. The present sequence is that of the human Akt1 protein

SQ Sequence 480 AA;

Query Match 99.8%; Score 2544; DB 4; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFYGYKRPQDVQREAPLNFSVAQC 60  
 Db 1 MSDVAIVKEGWLHKGRIYKTRPRYFLKNDGTFYGYKRPQDVQREAPLNFSVAQC 60  
 Qy 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREWTATQTVADGLKQEEEMDF 120  
 Db 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREWTATQTVADGLKQEEEMDF 120  
 Qy 121 RSGSPDSNGAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
 Db 121 RSGSPDSNGAEEMVSLAKPKHRVTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
 Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELPFHLS 240  
 Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELPFHLS 240  
 Qy 241 RERFSEDRAFYGAETVSALDYHSEKNVYRDLENLMDKDGHIKITDGLCKEGI 300  
 Db 241 RERFSEDRAFYGAETVSALDYHSEKNVYRDLENLMDKDGHIKITDGLCKEGI 300  
 Qy 301 KDGATMTFCGTPPYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
 Db 301 KDGATMTFCGTPPYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360  
 Qy 361 ILMEIIRFPRTLGPPEAKSLLSGLLKDPKQRLGGSEDAKEIMQHRFFAGIVQHVEYKK 420  
 Db 361 ILMEIIRFPRTLGPPEAKSLLSGLLKDPKQRLGGSEDAKEIMQHRFFAGIVQHVEYKK 420  
 Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDDDSMECVDSERRPHFPQFSYASGTA 480

|||||  
421 LSPPFKQVTSSETDTRYDEEFTAQMITITPPDQDDSMCEVDSERRPFPQFSYSASSTA 480

Db  
AAG67620  
AAG67620 standard; protein; 480 AA.

RESULT 9  
ID AAG67620 standard; protein; 480 AA.  
XX  
AC AAG67620;  
XX  
XX 26-NOV-2001 (first entry)  
XX  
XX Amino acid sequence of a human protein.  
XX  
XX Human; protein kinase; protein phosphatase; signal transduction.  
XX  
XX Homo sapiens.  
XX  
XX WO200109316-A1.  
XX  
XX 08-FEB-2001.  
XX  
XX 28-JUL-2000; 2000WO-JP005061.  
XX  
XX 29-JUL-1999; 99JP-00248036.  
XX  
XX 18-OCT-1999; 99US-0159590P.  
XX  
XX 11-JAN-2000; 2000JP-00118776.  
XX  
XX 17-FEB-2000; 2000US-0183322P.  
XX  
XX 02-MAY-2000; 2000JP-00183767.  
XX  
XX 09-JUN-2000; 2000JP-00241899.  
XX  
XX (HELI-) HELIX RES INST.  
XX  
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
XX  
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;  
XX  
XX Senoo C, Nezu J;  
XX  
XX WPI; 2001-570286/64.  
XX  
XX New genes encoding proteins with protein kinase/protein phosphatase  
XX  
XX activity, useful in the diagnosis and treatment of diseases.  
XX  
XX Example 4; Page 116-120; 233pp; Japanese.  
XX  
XX The specification describes human protein kinase/protein phosphatases. It  
XX  
XX is expected that the protein kinase/protein phosphatase gene participates  
XX  
XX in signal transduction in cells. The protein kinase/protein phosphatase  
XX  
XX polypeptides and polynucleotides are useful for developing diagnostics  
XX  
XX and treatment agents for human and animal diseases. The protein  
XX  
XX kinase/protein phosphatase polypeptides are useful as target molecules in  
XX  
XX designing novel drugs. The protein kinase/protein phosphatase  
XX  
XX polynucleotides are useful as a source of probes and primers, which may  
XX  
XX be used to isolate homologous sequences. The present sequence represents  
XX  
XX a human protein, which is used in the course of the invention  
XX  
XX Sequence 480 AA;  
XX  
XX Query Match 99.8%; Score 2544; DB 4; Length 480;  
XX  
XX Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
XX  
XX Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 MSDVAIVKGEHLKRGVYKTRPRYFLLKNDGTFYKRPQDVQDREAPLNFSVAQC 60  
XX  
XX 1 MSDVAIVKGEHLKRGVYKTRPRYFLLKNDGTFYKRPQDVQDREAPLNFSVAQC 60  
XX  
XX 61 QLMKTERPRNPTFIIRCLQWTVLIERFTHVTPPEREWTTAIQTVDGLKKQEEEMDF 120  
XX  
XX 61 QLMKTERPRNPTFIIRCLQWTVLIERFTHVTPPEREWTTAIQTVDGLKKQEEEMDF 120  
XX  
XX 121 RSGSPNSNGAEEMVSLAKPHRTVWNEFYLLKLGKTFGKVLVKEKATGRYAMKI 180  
XX  
XX 121 RSGSPNSNGAEEMVSLAKPHRTVWNEFYLLKLGKTFGKVLVKEKATGRYAMKI 180

181 LKKEVIIVAKDEVHTLTENRVLQNSRHPFLTALKYSPQTHDRLCFVMEYANGGELFFHLS 240  
181 LKKEVIIVAKDEVHTLTENRVLQNSRHPFLTALKYSPQTHDRLCFVMEYANGGELFFHLS 240  
241 RRVFSEDRARFYCAEIVSALDYHSEKNVYVYRDLEKLENLMLDKDGHIKITDFGLCKEGI 300  
241 RRVFSEDRARFYCAEIVSALDYHSEKNVYVYRDLEKLENLMLDKDGHIKITDFGLCKEGI 300  
301 KDGATMTFCGTPBYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFFYNQDHEKLPFEL 360  
301 KDGATMTFCGTPBYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFFYNQDHEKLPFEL 360  
361 ILMEERFPRPTLGPPEAKSLGGLKDPKORLGGSSDAKEIMOHRRFAGIVWQHVYK 420  
361 ILMEERFPRPTLGPPEAKSLGGLKDPKORLGGSSDAKEIMOHRRFAGIVWQHVYK 420  
421 LSPPFKQVTSSETDTRYDEEFTAQMITITPPDQDDSMCEVDSERRPFPQFSYSASSTA 480  
421 LSPPFKQVTSSETDTRYDEEFTAQMITITPPDQDDSMCEVDSERRPFPQFSYSASSTA 480

RESULT 10  
AAG67441  
ID AAG67441 standard; protein; 480 AA.  
XX  
AC AAG67441;  
XX  
XX 26-NOV-2001 (first entry)  
XX  
XX Amino acid sequence of a human polypeptide.  
XX  
XX Human; protein kinase; protein phosphatase; signal transduction;  
XX  
XX intracellular signalling pathway.  
XX  
XX Homo sapiens.  
XX  
XX WO200109345-A1.  
XX  
XX 08-FEB-2001.  
XX  
XX 28-JUL-2000; 2000WO-JP005060.  
XX  
XX 29-JUL-1999; 99JP-00248036.  
XX  
XX 18-OCT-1999; 99US-0159590P.  
XX  
XX 11-JAN-2000; 2000JP-00118776.  
XX  
XX 17-FEB-2000; 2000US-0183322P.  
XX  
XX 02-MAY-2000; 2000JP-00183767.  
XX  
XX (HELI-) HELIX RES INST.  
XX  
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
XX  
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;  
XX  
XX Senoo C, Nezu J;  
XX  
XX WPI; 2001-564736/63.  
XX  
XX New genes encoding protein kinase and protein phosphatase, useful for  
XX  
XX identifying modulators which can be used to treat human or animal  
XX  
XX disorders associated with the expression or function of these enzymes.  
XX  
XX Example 4; Page 218-221; 336pp; Japanese.  
XX  
XX The specification describes human protein kinase/protein phosphatases.  
XX  
XX The polypeptides are expected to participate in signal transduction in  
XX  
XX cells. The kinase phosphatases are connected with intracellular  
XX  
XX signalling pathways. Antisense oligonucleotides and compounds identified  
XX  
XX by screening (agonists or antagonists) can be used to treat human or  
XX  
XX animal disorders associated with the expression or function of the  
XX  
XX protein. In addition, the polypeptides may be used as target molecules  
XX  
XX for drug development. The present sequence represents a polypeptide, used  
XX  
XX in the course of the invention  
XX  
XX Sequence 480 AA;

|  |  |    |   |
|--|--|----|---|
| Query Match  | 99.8%; Score 2544; DB 4; Length 480;                                     | PS | Disclosure; Page 47-48; 53pp; English.                                    |
| Best Local Similarity  | 99.8%; Pred. No. 1.9e-234;   | XX | The invention relates to identifying an agent modulating interaction      |
| Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0; |  | CC | between integrin-linked kinase (ILK) and presenilin-1 (PS1) comprising    |
|  |  | CC | providing ILK, PS1 or their functional variants, as first and second      |
|  |  | CC | components respectively, contacting the components in the presence of a   |
|  |  | CC | test agent under conditions that in absence of the agent, would permit    |
|  |  | CC | the components to interact and determining whether the agent is capable   |
|  |  | CC | of modulating the interaction between the components. Also included are   |
|  |  | CC | the method above where the components are protein kinase beta (PKB),      |
|  |  | CC | gamma secretase or their functional variants, test kits for carrying out  |
|  |  | CC | the methods and an agent identified by the methods. The methods are used  |
|  |  | CC | for identifying an agent that modulates interaction between ILK and PS1.  |
|  |  | CC | or PKB or gamma-secretase. The agent has therapeutic applications in      |
|  |  | CC | treating humans or animals, for treating a host suffering from a          |
|  |  | CC | condition associated with an interaction between ILK and PS1, activity of |
|  |  | CC | PKB, activity of gamma-secretase, apoptosis, cancer and Alzheimer's       |
|  |  | CC | disease. The agent is also useful for manufacturing a medicament for use  |
|  |  | CC | in treatment of the above mentioned conditions. The present sequence      |
|  |  | CC | represents human protein kinase B alpha                                   |
|  |  | XX |   |
| SQ   | Sequence 480 AA;   |    |   |
| Query Match  | 99.8%; Score 2544; DB 5; Length 480;                                     |    |   |
| Best Local Similarity  | 99.8%; Pred. No. 1.9e-234;   |    |   |
| Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0; |  |    |   |
| Qy   | 1 MSDVAIVKEGWLHKGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60            |    |   |
| Db   | 1 MSDVAIVKEGWLHKGGEYIKTWPRYFLKNDGTFIGYKERPDVDQREAPLNFSVAQC 60            |    |   |
| Qy   | 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAQTVDGLKKQEEEMDF 120           |    |   |
| Db   | 61 QLMKTERPRNTFIIRCLQWTTVIERTFHVETPEEREETTAQTVDGLKKQEEEMDF 120           |    |   |
| Qy   | 121 RSGSPDNGSGAEEMVSLAKPKHRVTWNEPEYLLKLGKGTGKVLVKEKATGRYYAMKI 180        |    |   |
| Db   | 121 RSGSPDNGSGAEEMVSLAKPKHRVTWNEPEYLLKLGKGTGKVLVKEKATGRYYAMKI 180        |    |   |
| Qy   | 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240     |    |   |
| Db   | 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240     |    |   |
| Qy   | 241 RERVSEDRARFYGAEIVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300       |    |   |
| Db   | 241 RERVSEDRARFYGAEIVSALDYLHSEKNVYVRDLKLENMLDKDGHIKITDFGLCKEGI 300       |    |   |
| Qy   | 301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360        |    |   |
| Db   | 301 KDGATMKTFCGTPPYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYVQDHEKLFEL 360        |    |   |
| Qy   | 361 ILMEEIRFPRTLGPPEAKSLLSGLLKDPKQRLGGGSDAKEIMQHRFFAGIVMHOVVEKK 420      |    |   |
| Db   | 361 ILMEEIRFPRTLGPPEAKSLLSGLLKDPKQRLGGGSDAKEIMQHRFFAGIVMHOVVEKK 420      |    |   |
| Qy   | 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRPFPQFSYSASSTA 480      |    |   |
| Db   | 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRPFPQFSYSASSTA 480      |    |   |
| RESULT 11  |  |    |   |
| AAU79418   |  |    |   |
| ID   | AAU79418 standard; protein; 480 AA.                                      |    |   |
| XX   |  |    |   |
| AC   | AAU79418;  |    |   |
| XX   |  |    |   |
| DT   | 02-JUL-2002 (first entry)  |    |   |
| XX   |  |    |   |
| DE   | Human protein kinase B alpha.  |    |   |
| XX   |  |    |   |
| KW   | Human; integrin-linked kinase; ILK; presenilin-1; protein kinase B; PKB; |    |   |
| KW   | gamma secretase; apoptosis; Alzheimer's disease; PS-1; neurotropic;      |    |   |
| KW   | neuroprotective; cytostatic; cancer.                                     |    |   |
| XX   |  |    |   |
| OS   | Homo sapiens.  |    |   |
| XX   |  |    |   |
| FN   | WO200222862-A2.  |    |   |
| XX   |  |    |   |
| PD   | 21-MAR-2002.   |    |   |
| XX   |  |    |   |
| PF   | 12-SEP-2001; 2001WO-GB004094.  |    |   |
| XX   |  |    |   |
| PR   | 12-SEP-2000; 2000GB-00022333.  |    |   |
| XX   |  |    |   |
| PA   | (GLAX ) GLAXO GROUP LTD.   |    |   |
| XX   |  |    |   |
| PI   | Hiles ID, Ellis C;   |    |   |
| XX   |  |    |   |
| DR   | WPT; 2002-351896/38.   |    |   |
| XX   |  |    |   |
| PT   | Identifying agent that modulates interaction between integrin-linked     |    |   |
| PT   | kinase and presenilin-1, useful for treating Alzheimer's disease, and    |    |   |
| PT   | identifying agent that modulates protein kinase B or gamma secretase     |    |   |
| PT   | activity.  |    |   |
| XX   |  |    |   |



nonhyperlipidaemic; hypertension; vascular disease; gangrene; wound; Buerger's syndrome; myocardial infarction; coronary artery disease; ischaemia.

Homo sapiens.

Key Location/Qualifiers

Domain 5..108

/label= PH domain

/note= "Pleckstrin homology domain"

Domain 150..408

/note= "Kinase domain"

Modified-site 308

/note= "Phosphorylation site"

Modified-site 473

/note= "Phosphorylation site"

WO200193806-A2.

13-DEC-2001.

05-JUN-2001; 2001WO-US018175.

08-JUN-2000; 2000US-00590740.

(SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.

Walsh K;

WPI; 2002-164293/21.

N-PSDB; AAD28548.

Use of 3-hydroxy-3-methylglutaryl-coenzyme A reductase inhibitor in promoting angiogenesis in a tissue of a subject to treat conditions e.g. hypertension.

Disclosure; Page 66-67; 70pp; English.

The invention relates to 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase inhibitors and their use in promoting angiogenesis and in activating Akt polypeptides in vascular endothelial cells. Akt is a proto-oncogene encoding a serine-threonine kinase (also known as protein kinase B, PKB). The invention also relates to methods and compositions for the treatment of conditions associated with vascular insufficiency. HMG-CoA reductase inhibitors are used for treating nonhyperlipidaemic and/or nonhypercholesterolaemic subjects who are in need of increased blood flow to a tissue or promoting angiogenesis, to treat conditions such as hypertension, diabetic peripheral vascular disease, gangrene, Buerger's syndrome, wound (e.g. surgical wound), ischaemia of the muscle, brain, kidney, lung, heart and limb, severe occlusive and/or obstructive vascular disease, peripheral vascular disease, myocardial ischaemia, myocardial infarction, coronary artery disease, cerebral vascular disease and visceral vascular disease. The present sequence is human Akt protein

Sequence 480 AA;

Query Match 99.8%; Score 2544; DB 5; Length 480;

Best Local Similarity 99.8%; Pred. No. 1.9e-234;

Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MSDVAIVKGEWHLKRGVYIKTRPRYFLKNDGTFIGYKRPQDVQDQREAPLNNFSAQC 60

1 MSDVAIVKGEWHLKRGVYIKTRPRYFLKNDGTFIGYKRPQDVQDQREAPLNNFSAQC 60

61 QLMKTERPRNTFIIRCLQWTVTERTFHVTPPEREWTTAIQTVADGLKKQEEEMDF 120

61 QLMKTERPRNTFIIRCLQWTVTERTFHVTPPEREWTTAIQTVADGLKKQEEEMDF 120

121 RSGSPDSNGAEEMVSLAKPKHVRVWNEFYLLKLGKGTGKVLVKEKATGRYAMKI 180

121 RSGSPDSNGAEEMVSLAKPKHVRVWNEFYLLKLGKGTGKVLVKEKATGRYAMKI 180

181 LKKEVIVAKDEVVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGBELFFHLS 240

Db 181 LKKEVIVAKDEVVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGBELFFHLS 240

Qy 241 RERVFSDDRARFYGAETVSALDYLHSEKNVYVYRDLEKLENMLDKDGHKIKITDFGLCKEGI 300

Db 241 RERVFSDDRARFYGAETVSALDYLHSEKNVYVYRDLEKLENMLDKDGHKIKITDFGLCKEGI 300

Qy 301 KDGMTKTCCTPEYLAPEVLENDNDYGRVDWGLGVVYEMMCGRLPFFYNQDHEKLPFEL 360

Db 301 KDGMTKTCCTPEYLAPEVLENDNDYGRVDWGLGVVYEMMCGRLPFFYNQDHEKLPFEL 360

Qy 361 ILMEEIFRPTLGPPEAKSLLSGLLKDPKORLGGGSEDAKEIMQHRFFAGVWQHVYKK 420

Db 361 ILMEEIFRPTLGPPEAKSLLSGLLKDPKORLGGGSEDAKEIMQHRFFAGVWQHVYKK 420

Qy 421 LSPPFKQVTSSETDTRYDFDEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSASGTA 480

Db 421 LSPPFKQVTSSETDTRYDFDEFTAQMITITPPDQDDSMCEVDSERRRPHFPQFSASGTA 480

RESULT 13

ABB06996

ID ABB06996 standard; protein; 480 AA.

XX AC ABB06996;

XX DT 20-JUN-2002 (first entry)

XX DE Human Akt1 protein SEQ ID NO:5.

XX KW Human; Hsp90 beta; Hsp90 alpha; Akt1; Akt2; Akt3; apoptosis regulation; apoptosis; serine/threonine kinase; heat shock protein; anticancer; cytosolic; cardiant; vasotropic; hepatotropic; neuroprotective; antidiabetic; nootropic; cancer; diabetes; Alzheimer's disease; cell death; radiation; brain ischaemia; cardiac ischaemia.

XX OS Homo sapiens.

XX PN WO200215925-A1.

XX PD 28-FEB-2002.

XX PF 22-AUG-2001; 2001WO-JP007179.

XX PR 22-AUG-2000; 2000JP-00251529.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX TSURUO T.

XX PI Tsuruo T, Fujita N, Sato S;

XX DR WPI; 2002-292035/33.

XX DR N-PSDB; ABL50837.

XX PT Regulation of apoptosis by promoting or inhibiting the intracellular binding of Akt with Hsp90, useful for prevention and treatment of apoptosis-regulation associated diseases including cancer.

XX PS Claim 12; Page 76-78; 93pp; Japanese.

XX CC The present invention describes the regulation of apoptosis, in which the intracellular binding of Akt (a serine/threonine kinase) with Hsp90 (a heat-shock protein) is promoted or inhibited. The present invention also describes: (1) isoforms of Akt and Hsp90, and their partial peptides including the binding domain; (2) antibodies to Akt or Hsp90; (3) DNA encoding Akt or Hsp90 or their partial peptides including the binding domain; (4) expression vectors containing the DNA; (5) host cells transformed by the vectors; (6) production of Akt or Hsp90 or their partial peptides including the binding domain by culture of the transformed cells; (7) screening compounds for their ability to modify intracellular Akt activity by contact with cells expressing Akt or Hsp90; and (8) drug compositions containing antibodies recognizing the binding domain of Akt or Hsp90 and optionally also an anticancer agent. Akt and

CC Hsp90 have cytosolic, cardiac, vasotropic, hepatotropic, antidiabetic,  
 CC neuroprotective and neurotropic activities. Blockade of the binding of  
 CC Hsp90 with Akt increases the sensitivity of cells to apoptosis induction.  
 CC Akt and Hsp90 can be used in the prevention and treatment of diseases  
 CC with which apoptosis regulation is associated, including cancer (such as  
 CC gastric cancer, ovarian cancer, breast cancer, pancreatic cancer and  
 CC prostate cancer), diabetes, Alzheimer's disease, cell death caused by  
 CC radiation or anticancer agents, brain ischaemia or cardiac ischaemia. The  
 CC present sequence represents human Akt1 which is used in the  
 CC exemplification of the present invention

XX Sequence 480 AA;

Query Match 99.8%; Score 2544; DB 5; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKGEWHLKRGYIKTWPRYFLKNDGTFIGYKRPQDVQREAPLNFSVAQC 60  
 Db 1 MSDVAIVKGEWHLKRGYIKTWPRYFLKNDGTFIGYKRPQDVQREAPLNFSVAQC 60  
 Qy 61 QLMKTERPRNPTFIIRCLQWTVIERTFHVETPEEREETTAQTQVADGLKKQEEEMDF 120  
 Db 61 QLMKTERPRNPTFIIRCLQWTVIERTFHVETPEEREETTAQTQVADGLKKQEEEMDF 120  
 Qy 121 RSGSPSDNSGAEMEVSIAKPKHRTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
 Db 121 RSGSPSDNSGAEMEVSIAKPKHRTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
 Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFTQHDRLCFVMEYANGSELFPFHL 240  
 Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFTQHDRLCFVMEYANGSELFPFHL 240  
 Qy 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDGLCKEGI 300  
 Db 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDGLCKEGI 300  
 Qy 301 KDGATMKTFCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFEL 360  
 Db 301 KDGATMKTFCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFEL 360  
 Qy 361 ILMBEIRPRTLGLPEAKSLLSGLLKQPKQKRLGGSEDAKEIMQHRFFAGIVQHVYVEKK 420  
 Db 361 ILMBEIRPRTLGLPEAKSLLSGLLKQPKQKRLGGSEDAKEIMQHRFFAGIVQHVYVEKK 420  
 Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDSDMECVDSRRPHFPQFSYASGTA 480  
 Db 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDSDMECVDSRRPHFPQFSYASSTA 480

RESULT 14

ID ABR57472 standard; protein; 480 AA.

XX ABR57472;

XX 15-SEP-2003 (first entry)

DT Human PKB-alpha amino acid sequence.

DE Protein kinase B; PKB/Akt; enzyme; crystal structure; drug discovery;  
 DE protein co-ordinate data; cytosolic; antidiabetic; vasotropic; PKB;  
 DE neurotropic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;  
 DE structural analysis; cancer; diabetes; diabetes; erectile dysfunction; human;  
 DE neurodegeneration.

XX Homo sapiens.

XX WO2003016516-A2.

PN 27-FEB-2003.

XX 14-AUG-2002; 2002WO-GB003735.

XX 14-AUG-2001; 2001GB-00019860.  
 PR 01-MAY-2002; 2002GB-00009985.  
 XX (NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.  
 PA (CANC-) CANCER RES INST.  
 XX Barford D, Yang J, Hemmings BA, Cron PD;  
 XX WPI; 2003-268328/26.

XX New crystal of protein kinase B beta, useful for activating protein  
 PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates  
 PT or a tetragonal space group.

XX Disclosure; Fig 7; 284pp; English.

XX The present invention describes a crystal of protein kinase B beta  
 CC (PKBbeta) comprising (i), where (i) comprises: (a) a tetragonal space  
 CC group P4-1-2-1-2 and unit cell dimensions of: a = 149.33 plus or minus  
 CC 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or  
 CC minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40  
 CC plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =  
 CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom,  
 CC c = 39.19 plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5  
 CC Angstrom, b = 149.52 plus or minus 0.5 Angstrom, c = 39.06 plus or minus  
 CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in  
 CC the specification. (i) has cytostatic, antidiabetic, vasotropic,  
 CC neurotropic and neuroprotective activities, and can be used in gene  
 CC therapy. The crystal of PKBbeta, and methods from the present invention,  
 CC are useful in activating protein kinases, particularly AGC kinases, for  
 CC identifying modulators of protein kinase activity, and for structural  
 CC analysis of other protein kinases. The crystal may also be used in  
 CC manufacturing a medicament for treating cancers, diabetes, erectile  
 CC dysfunction or neurodegeneration. The present sequence represents the  
 CC human PKB-alpha amino acid sequence, which is given in the  
 CC exemplification of the present invention

XX Sequence 480 AA;

Query Match 99.8%; Score 2544; DB 6; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSDVAIVKGEWHLKRGYIKTWPRYFLKNDGTFIGYKRPQDVQREAPLNFSVAQC 60  
 Db 1 MSDVAIVKGEWHLKRGYIKTWPRYFLKNDGTFIGYKRPQDVQREAPLNFSVAQC 60  
 Qy 61 QLMKTERPRNPTFIIRCLQWTVIERTFHVETPEEREETTAQTQVADGLKKQEEEMDF 120  
 Db 61 QLMKTERPRNPTFIIRCLQWTVIERTFHVETPEEREETTAQTQVADGLKKQEEEMDF 120  
 Qy 121 RSGSPSDNSGAEMEVSIAKPKHRTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
 Db 121 RSGSPSDNSGAEMEVSIAKPKHRTWNEPEYLLKLGKTFGKVLVKEKATGRYYAMKI 180  
 Qy 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFTQHDRLCFVMEYANGSELFPFHL 240  
 Db 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFTQHDRLCFVMEYANGSELFPFHL 240  
 Qy 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDGLCKEGI 300  
 Db 241 RERVSEDRARFYGAIEVSALDYHSEKNVYVRDLKLENMLDKDGHKIKITDGLCKEGI 300  
 Qy 301 KDGATMKTFCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFEL 360  
 Db 301 KDGATMKTFCGTPPEYLAPEVLENDYGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFEL 360  
 Qy 361 ILMBEIRPRTLGLPEAKSLLSGLLKQPKQKRLGGSEDAKEIMQHRFFAGIVQHVYVEKK 420  
 Db 361 ILMBEIRPRTLGLPEAKSLLSGLLKQPKQKRLGGSEDAKEIMQHRFFAGIVQHVYVEKK 420  
 Qy 421 LSPFPKQVTSSETDTRYFDEEFTAQMITITPPDQDSDMECVDSRRPHFPQFSYASGTA 480

Db 421 LSPFPKQVTSYDTRFDDEFTAQMITITPPDQDDSMCEVDSRRPHFPQFSASSTA 480

RESULT 15  
ADFI18630  
ID ADFI18630 standard; protein; 480 AA.  
XX ADFI18630;  
AC ADFI18630;  
XX 12-FEB-2004 (first entry)  
DT Human Akt kinase.  
XX Human Akt kinase.  
DE Human; Akt; oncoprotein E7; cytostatic; gene therapy; kinase; enzyme.  
KW Homo sapiens.  
XX WO2003088922-A2.  
XX 30-OCT-2003.  
XX 21-APR-2003; 2003WO-US012667.  
XX 19-APR-2002; 2002US-0374245P.  
XX (UTRP ) UNIV ROCHESTER.  
XX McCance D, Westbrook TF;  
PI WPI; 2003-845498/78.  
DR N-PSDB; ADFI18631.  
XX

Identifying a compound that inhibits E7 cellular proliferation activity by administering a compound to a system, where the system maintains Akt activity and selecting a compound that decreases the amount of Akt activity.  
PS Disclosure; SEQ ID NO 6; 119pp; English.  
XX The present sequence is the protein sequence of human Akt. This is a kinase that phosphorylates p21Cip1 in the nuclear localisation signal of p21Cip1. Upon phosphorylation, nuclear transport does not occur and p21Cip1 is ubiquitinated and subsequently degraded. Human papillomavirus oncoprotein E7 abrogates Raf-associated arrest and prevents inhibition of cyclin E-CDK2 activity without disrupting Raf induction of p21Cip1. E7 neither interacts with p21Cip1 nor derepresses p21Cip1-associated CDK2 activity, but instead reduces the association between p21Cip1 and cyclin E-CDK2 complexes. Raf down-regulates steady-state levels of Akt, a regulator of p21Cip1 localisation, leading to loss of p21Cip1 phosphorylation and accumulation of p21Cip1. E7 disrupts the effects of Raf on Akt activity and prevents p21Cip1 nuclear accumulation. Maintenance of Akt activity is necessary and sufficient to bypass Raf arrest. The invention provides methods for identifying and using inhibitors of E7 cell proliferation activity, and for identifying and using compounds capable of promoting the nuclear localization of p21Cip1. The methods can be used to inhibit aberrant cellular proliferation for treatment of cancer.

XX Sequence 480 AA;  
SQ  
Query Match 99.8%; Score 2544; DB 7; Length 480;  
Best Local Similarity 99.8%; Pred. No. 1.9e-234;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MSDVAIVKEGWHLKGEYIKTWRRPYELLKNDGTFYKRPQDDVDQREAPLNFSVAQC 60  
DB 1 MSDVAIVKEGWHLKGEYIKTWRRPYELLKNDGTFYKRPQDDVDQREAPLNFSVAQC 60  
QY 61 QLMKTERPRPNTFIIRCLQWTVIERTFHVETPEEREETWTAIQTVADGLKKQEEEMDF 120  
DB 61 QLMKTERPRPNTFIIRCLQWTVIERTFHVETPEEREETWTAIQTVADGLKKQEEEMDF 120

QY 121 RSGSPSDNSGAEEMEVSILAKPKHRVTWNEPEYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
DB 121 RSGSPSDNSGAEEMEVSILAKPKHRVTWNEPEYLLKLGKGTGKVLVKEKATGRYYAMKI 180  
QY 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
DB 181 LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS 240  
QY 241 RERVPSDRARFYGAIEIVSALDYLHSEKNVYVYRDLKLENMLDKDGHIKITDFGLCKEGI 300  
DB 241 RERVPSDRARFYGAIEIVSALDYLHSEKNVYVYRDLKLENMLDKDGHIKITDFGLCKEGI 300  
QY 301 KDGMTKTFCTGTPYLAPEVLENDYGRAVDWGLGVVMEYMMCGRLPFYVQDHEKLFEL 360  
DB 301 KDGMTKTFCTGTPYLAPEVLENDYGRAVDWGLGVVMEYMMCGRLPFYVQDHEKLFEL 360  
QY 361 ILMEIIRFPRTLGPPEAKSLLSGLLKQPKQRLGGSGSEDAKEIMQHRFPFAGIVMQHYEKK 420  
DB 361 ILMEIIRFPRTLGPPEAKSLLSGLLKQPKQRLGGSGSEDAKEIMQHRFPFAGIVMQHYEKK 420  
QY 421 LSPFPKQVTSYDTRFDDEFTAQMITITPPDQDDSMCEVDSRRPHFPQFSASSTA 480  
DB 421 LSPFPKQVTSYDTRFDDEFTAQMITITPPDQDDSMCEVDSRRPHFPQFSASSTA 480

Search completed: February 23, 2005, 20:45:26  
Job time : 168 secs

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